

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 10:03:29 ; Search time 4879 Seconds  
(without alignments)  
10447.101 Million cell updates/sec

Title: US-10-626-445-5  
Perfect score: 1176  
Sequence: 1 atgtcggagttaacagctac.....accagtcagtattcttctga 1176

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_ov.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_on.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_hgt\_hum.\*

31: em\_hgt\_inv.\*

32: em\_hgt\_inv.\*

33: em\_hgt\_mus.\*

34: em\_hgt\_pln.\*

35: em\_hgt\_rod.\*

36: em\_hgt\_nam.\*

37: em\_hgt\_vrt.\*

38: em\_sv.\*

39: em\_higo\_hum.\*

40: em\_higo\_mus.\*

41: em\_higo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1176	100.0	1538	10	AF358859	Mus muscu
2	958.4	81.5	1593	10	AF358860	Rattus no
3	821.4	69.8	200346	2	AC131672	Mus muscu
4	686.6	58.4	1173	6	AR142850	Sequence
5	686.6	58.4	1173	6	AR391860	Sequence
6	686.6	58.4	1173	6	AX109119	Sequence
7	686.6	58.4	1173	6	AX139113	Sequence
8	686.6	58.4	1173	6	BD015847	Novel pol
9	686.6	58.4	1173	9	AF325356	Homo sapi
10	686.6	58.4	1173	9	AF329449	Homo sapi
11	686.6	58.4	1173	9	AY008280	Homo sapi
12	686.6	58.4	1173	9	AY136745	Homo sapi
13	686.6	58.4	1173	9	HS298292	Homo sapi
14	686.6	58.4	1266	6	AX376577	Sequence
15	686.6	58.4	1300	6	AX301229	Sequence
16	686.6	58.4	1312	6	BD095598	Novel gua
17	686.6	58.4	1312	9	AB045370	Homo sapi
18	686.6	58.4	3689	6	AX549343	Sequence
19	686.6	58.4	3689	9	AF312230	Homo sapi
20	685	58.2	1227	6	BD097512	Novel gua
21	685	58.2	1265	9	AB044934	Homo sapi
22	683.4	58.1	1173	6	AX301763	Sequence
23	683.4	58.1	1173	9	AF307973	Homo sapi
24	651	55.4	236694	2	AC118386	Rattus no
25	621.4	52.8	1291	4	AB053300	Sus scrof
26	613	52.1	1451	10	AF358858	Cavia por
27	442	37.6	140555	9	AC007922	Homo sapi
28	442	37.6	166206	2	AC009668	Homo sapi
29	442	37.6	167296	2	AP002507	Homo sapi
30	442	37.6	169144	9	AC090244	Homo sapi
31	442	37.6	184938	2	AP002476	Homo sapi
32	442	37.6	193779	2	AP001327	Homo sapi
33	271.6	23.1	1326	6	AX451922	Sequence
34	178	15.1	1249	10	AF267538	Cavia por
35	172.8	14.7	1239	6	E39806	Novel guano
36	172.8	14.7	1242	10	AY009371	Rattus no
37	172.8	14.7	2700	6	E39809	Novel guano
38	150.8	12.8	1339	10	AF267537	Cavia por
39	145.4	12.4	18105	6	BD189979	Use of hi
40	143.8	12.2	2067	10	AY142145	Mus muscu
41	143.8	12.2	2483	10	AY044153	Mus muscu
42	143.2	12.2	1335	10	AF237919	Rattus no
43	143.2	12.2	1338	6	AR104204	Sequence
44	143.2	12.2	1338	6	BD086288	G protein
45	143.2	12.2	1338	10	AY009370	Rattus no

# ALIGNMENTS

RESULT 1  
AF358859  
LOCUS AF358859 1538 bp mRNA linear ROD 02-SEP-2001  
DEFINITION Mus musculus histamine H4 receptor mRNA, complete cds.  
ACCESSION AF358859  
VERSION AF358859.1 GI:15420534  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1. (bases 1 to 1538)  
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
Comparison of human, mouse, rat, and guinea pig histamine H4  
receptor suggests substantial species variation



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ORIGIN
Query Match      81.5%; Score 958.4; DB 10; Length 1593;
Best Local Similarity 88.4%; Pred No. 1.5e-260;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1  ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAAGTGTCTCAGTCCCTTGGCATTT 60
DB 36  ATGTCGGAGTCTAACGGCACTGACGCTCTGCCACTGACTGTCTCAAGTCCCTTGGCATTT 95
QY 61  TTAATGCTCTCATTTGCTTTGCTATATAGTGGCAATGCTGTGCTATCTTAGCCTTT 120
DB 96  TTAATGCTCCCTGCTTGTCTTGTCTATAAGTAGGCAATGCTGTGCTATCTTAGCCTTT 155
QY 121  GTGGTGGACAGAACTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
DB 156  GTAGCAGACAGAACTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 215
QY 181  GACTTCCTCGTGGGTTTGAATTTCCATCTCTGTATACATCCCTCAAGTGTGTTAACTGG 240
DB 216  GACTTCCTCGTGGGTTTGAATTTCCATCTCTGTATACATCCCTCAAGTGTGTTAACTGG 275
QY 241  AATTTTGAAGTGGAACTGCAATGTTTGGCTCAATCTACTGACTATCTTTTGGCAAGCA 300
DB 276  AATTTTGAAGTGGAACTGCAATGTTTGGCTCAATCTACTGACTATCTTTTGGCAAGCA 335
QY 301  TCTGCTCTACAATATGTCCTCATTAAGTACGATCGATACGATCGATTTCAATGCTGTG 360
DB 336  TCCGCTCTACAGTATGTCCTCATTAAGTACGATCGATCGATCGATTTCAATGCTGTG 395
QY 361  TCTTATAGGCTCAACACACTGGCATCAATGAAGATTTGTCCTCAATGTCGCTGTTGG 420
DB 396  CGTTATAGACACACACTGGCATCGTGAATTTGTCCTCAATGTCGCTGTTGG 455
QY 421  ATACTGGCTTTCTTGGTAAATGGCCGATGATCTGGCTTCAGATCTTGGAAAGACAGC 480
DB 456  ATACTGGCTTTCTTGGTAAATGGCCGATGATCTGGCTTCAGATCTTGGAAAGACAGC 515
QY 481  ACGAAACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCCACCATACA 540
DB 516  ACCAACACAGAGAGTGGAGCTGGCTTTGTTACAGAGTGGTACATCTCCACCATACA 575
QY 541  ATGCTCTTGAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 576  GCATTTCTTGAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 635
QY 601  TGGAGCTGTGAAGGTTAGGCTCTCAGTAGGTGCCCTAGCCATGCTGATTTCCACT 660
DB 636  TGGAGCTGTGAAGGTTAGGCTCTCAGTAGGTGCCCTAGCCATGCTGATTTCCACT 695
QY 661  ACTCTCTTCCAGTCTTACAGACACTTACACAGAGTGGGCTGGCTGTCAGGACAGTAAT 720
DB 696  ACTCTCTTCCAGGCTCTGACACTACACAGAACTGGGCTGGCTGTCAGGACAGTCTT 755
QY 721  CTGGATTAAGAAATFAGCTGCATCTGCTCACTCAGAAAGTCTTCAAGAAAGAGCAGC 780
DB 756  CTGGATTAAGAAATFAGCTGCATCTGCTCACTCAGAAAGTCTTCAAGAAAGAGCAGC 815
QY 781  ATCCTGGTCTCTTAAGGACTACATGAACAGAGTATCACTGCCTTCAAGTGGTTCC 840
DB 816  CTCCTGGTCTCTTAAGGACTACATGAACAGAGTATCACTGCCTTCAAGTGGTTCC 875
QY 841  TTCTGCGATCGAAAGTGCAGGCTTCGCCAAAGGAGTAGCAGAGCTTCTCAGAGC 900
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DB 876  TTCTCCGATCAGAAAGCCAGTCTTCCACAGAGAGACAGTGGAGCTTCTCAGAGGC 935
QY 901  AGGAAGCTAGCAGAGTCTACTGCCATCTCTTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
DB 936  AGGAAGCTAGCAGAGTCTACTGCCATCTCTTGAGCGCTTTTGCCATTTGCTGGGCTCGG 995
QY 961  TACTGTCTGTTTACAAATTTGCTTTCACTTTACCCAGAACGGAACGCCCAAAATCGGTG 1020
DB 996  TATTGCCCTGTTTACAAATTTGCTTTCACTTTATCCAGAGGAGCGGCCCAAAATCGATT 1055
QY 1021  TGGTACAGCATTTGCTTCTGCTGCAATGGTTCATTTGTTTAAATCCCTTTCTGTAC 1080
DB 1056  TGGTACAGCATTTGCTTCTGCTGCAATGGTTCATTTGTTTAAATCCCTTTCTGTAC 1115
QY 1081  CTTTGTGTCTACAGCGCTTTCCAGAGGCTTTCTGGAAGATACCTTTGTGTGCAAGCAA 1140
DB 1116  CTTTGTGTCTACAGCGCTTTCCAGAGGCTTTCTGGAAGATACCTTTGTGTGCAAGCAA 1175
QY 1141  CCAGGCTGTCTACAGAACGAGTCAGTATCTTCTTGA 1176
DB 1176  CCAGGCTGTCTACAGAACGAGTCAGTATCTTCTTGA 1211

RESULT 3
AC131672/c
LOCUS          200346 bp      DNA      linear      HTG 06-NOV-2003
DEFINITION    Mus musculus chromosome UNK clone RP23-314021, WORKING DRAFT
ACCESSION     AC131672
VERSION       AC131672.2  GI:38194370
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     1 (bases 1 to 200346)
AUTHORS       Wilson,R.K.
TITLE         The sequence of Mus musculus clone
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 200346)
AUTHORS       McPherson,J.D. and Waterston,R.H.
TITLE         Direct Submission
JOURNAL       Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park
REFERENCE     3 (bases 1 to 200346)
AUTHORS       Wilson,R.K.
TITLE         Direct Submission
JOURNAL       Submitted (06-NOV-2003) Genome Sequencing Center, 4444 Forest Park
COMMENT       On Nov 6, 2003 this sequence version replaced gi:22475584.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA0314021
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 199211 bases at least Q40
Consensus quality: 199561 bases at least Q30
Consensus quality: 199715 bases at least Q20
Insert size: 199000; agarose-fp
Quality coverage: 13.37 in Q20 bases; agarose-fp
Quality coverage: 11.03 in Q20 bases; sum-of-contigs
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\* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 1 56: contig of 56 bp in length  
\* 57 156: gap of unknown length  
\* 1270: contig of 1114 bp in length  
\* 1370: gap of unknown length  
\* 1371 85906: contig of 84536 bp in length  
\* 85907 86006: gap of unknown length  
\* 86007 200346: contig of 114340 bp in length.

## FEATURES

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1. .200346  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/chromosome="UNK"  
/clone="RP23-314021"  
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157. .1270  
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1371. .85906  
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misc\_feature

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misc\_feature

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misc\_feature

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## ORIGIN

Query Match 69.8%; Score 821.4; DB 2; Length 200346;

Best Local Similarity 95.9%; Pred. No. 1.1e-221; Matches 843; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 298 GCATCTGTACAAATATTGCTCCTCAATAGCTACGATCGATACGATCGATGCTTCAAAATGCT 357  
Db 93779 GCATATCCCTGGAACATGTGTGTTTTCATTAAACACCATAGTTGCTCTGGTTCTTTAG 93720  
Qy 358 GTGCTTTATAGGCTCAACACACTGGCATCATGATGAGATTGTTGCTCAAAATGGTGGCTGTT 417  
Db 93719 GTGCTTTATAGGCTCAACACACTGGCATCATGATGAGATTGTTGCTCAAAATGGTGGCTGTT 93660  
Qy 418 TGGATCTGCTTCTTGGTAAATGGCCGATGATCTGCTTCAGATTCTTGGAAAGAC 477  
Db 93659 TGGATCTGCTTCTTGGTAAATGGCCGATGATCTGCTTCAGATTCTTGGAAAGAC 93600  
Qy 478 AGCAGCAACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGTACATCCTCACCAT 537  
Db 93599 AGCAGCAACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGTACATCCTCACCAT 93540  
Qy 538 ACATGCTCTTGGAAATCCCTGCTTCCTGCTCATCTCTGCTGCTTATTTCAATGTACAGATT 597  
Db 93539 ACATGCTCTTGGAAATCCCTGCTTCCTGCTCATCTCTGCTGCTTATTTCAATGTACAGATT 93480  
Qy 598 TACTGGAGCCTGTGGAAGCCTAGGCTCTCAGTAGGTGCTTACAGCCTAGCCTGCTGATTTCTCC 657  
Db 93479 TACTGGAGCCTGTGGAAGCCTAGGCTCTCAGTAGGTGCTTACAGCCTAGCCTGCTGATTTCTCC 93420  
Qy 658 ACTACCTCTTCCAGTGTCTCAGACACTTACAGAGCTGGGTGGGTTCAGAGCAAGT 717  
Db 93419 ACTACCTCTTCCAGTGTCTCAGACACTTACAGAGCTGGGTGGGTTCAGAGCAAGT 93360  
Qy 718 AATCTCGATTGAAGAACTCAGCTGCTGCTCACTCAGAAAGTCTTCGAAAGAGAGC 777  
Db 93359 AATCTCGATTGAAGAACTCAGCTGCTGCTCACTCAGAAAGTCTTCGAAAGAGAGC 93300  
Qy 778 AGCATCTGTGTCTTAAAGACTCACATGAACAGAGTATCACTGCTTTCAAAGTGGGT 837  
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Db 93239 TCCTTCTGGCGATCGGAAAGTGCAGCGCTTCGCGAAAGGAGTACGAGAGCTTCTCAGA 93180  
Qy 898 GGCAGGAAGCTAGCAGGTACAGGTACAGGTACAGGTACAGGTACAGGTACAGGTACAGGTACAGGT 957  
Db 93179 GGCAGGAAGCTAGCAGGTACAGGTACAGGTACAGGTACAGGTACAGGTACAGGTACAGGTACAGGT 93120  
Qy 958 CCATACCTGTCTGTTCACAATTCCTTCAACTTACCCAGAACGCGCCCAAAATCG 1017  
Db 93119 CCATACCTGTCTGTTCACAATTCCTTCAACTTACCCAGAACGCGCCCAAAATCG 93060  
Qy 1018 GTGTGGTACAGCAATGCTTCTGCTGCTCAATGGTTCAAATTCGTTTGTAAATCCCTTCTG 1077  
Db 93059 GTGTGGTACAGCAATGCTTCTGCTGCTCAATGGTTCAAATTCGTTTGTAAATCCCTTCTG 93000  
Qy 1078 TACCTTTGTGTACAGGCGTTTCCAGAGGCTTCTGGAAGATACATTTGTGTGACAAAG 1137  
Db 92999 TACCTTTGTGTACAGGCGTTTCCAGAGGCTTCTGGAAGATACATTTGTGTGACAAAG 92940  
Qy 1138 CAACGAGCGTGTACAGAACCACTGATATCTTCTTGA 1176  
Db 92939 CAACGAGCGTGTACAGAACCACTGATATCTTCTTGA 92901

## RESULT 4

AR142850

LOCUS

AR142850

DEFINITION

Sequence 1 from patent US 6204017.

ACCESSION

AR142850

VERSION

AR142850.1

GI:15104136

KEYWORDS

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 1173)

AUTHORS

Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L., Umland, S.P. and Wang, S.

TITLE

Polynucleotide encoding a histamine receptor

JOURNAL

Patent: US 6204017-A 1 20-MAR-2001;

FEATURES

Location/Qualifiers

1. .1173

/organism="unknown"

/mol\_type="unassigned DNA"

## ORIGIN

Query Match 58.4%; Score 686.6; DB 6; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 2e-183;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGAGTCTAACAGTACTGGCATCTGCCACCACTGCTCAGGTCCCTTGGCAATT 60  
Db 1 ATGCCAGATCTAATAGCAACAATTTATCACTAAGCACTCGTGTACTTTAGCAATT 60  
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Db 61 TTTATGTCCTTAGTAGCTTTGCTATAATGCTAGGAATGCTTTGCTCACTTTAGCTTTT 120  
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Db 421 GTGCTGGCTCTTCTAGTGAATGGCCAAATGATCTAGTTTTCAGAGCTTGGGAAGGA- 476
QY 481 ACGAACACAAAGACTGTGAGCTGCTTGTGTACAGAGTGGTACATCTCCACCATACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTGCATACA 534
QY 541 ATGCTCTTGAATTCCTGCTTCTGTCATCTCTGTGCTTATTTCAATGTACAGATTTC 600
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QY 601 TGGAGCTGTGGAAGCGTAGGGCTCTCAGTGTGCTGCTAGCCATCTGGATTTCTCCACT 660
Db 595 TGGAGCTGTGGAAGCGTGATCATCTCAGTGTGCTGCTAGCCATCTCTGACTGCTGCT 654
QY 661 ACTCTTCCAGTCTTTCAGGACCTTACAGAGCTGGGGTGGCTTGCAGGACAAATAAT 720
Db 655 GTCTCTTCAACATCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714
QY 721 CTGGAATGAAGGAATCAGCTGCTCATCTCGTCACTCAGAAAGTCTCTCGAAAGAGCAGC 780
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Db 1135 CCTCTACCATCAACACAGCTCGGTGATCTCTCTTAA 1173
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RESULT 5
AR391860
LOCUS 1173 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6613533.
ACCESSION AR391860
VERSION AR391860.1 GI:40115588
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monisma,F.J., Morse,K.L.,
Umland,S.P. and Wang,S.
TITLE Histamine receptor
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;
FEATURES Location/Qualifiers
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Source 1. .1173
/organism="unknown"
/mol_type="genomic DNA"

Query Match 58.4%; Score 686.6; DB 6; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-183;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

ORIGIN
1 ATGTCGAGTCTAAACAGTACTGGCATCTGGCCACACAGCTGCTCAGTCCCTTGGCAATTT 60
Db 1 ATGCCAGATACATAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAAT 60
QY 61 TTAATGCTCTTCAATTTGCCCTTTCGTATAATGTTAGGCAATGCTGTGCTCATCTTAGCCT 120
Db 61 TTTATGCTCTTAGTAGCTTTTGTATAATGCTAGGAAATGCTTTGTGCTCATTTTAGCTTT 120
QY 121 GTGGTGCACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
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QY 421 ATACTGCTTCTTGTGTAATGSCCGATGATTTCTGCTTCAATTTCTGATTTCTTGAAGAACAGC 480
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DEFINITION Sequence 1 from Patent WO0125432.
ACCESSION AXI09119
VERSION AXI09119.1 GI:13924093
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Umland,S. and Wang,S.
TITLE Histamine receptor
JOURNAL Patent: WO 0125432-A 1 12-APR-2001;
SCHERING CORPORATION (US)
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Best Local Similarity 75.1%; Pred. No. 2e-183;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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DEFINITION Sequence 1 from Patent EP1096009.
ACCESSION AXI39113
VERSION AXI39113.1 GI:14274791
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Peter,B. and O'Reilly,M.A.
TITLE G-protein coupled receptor-like polypeptide
JOURNAL Patent: EP 1096009-A 1 02-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
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Query Match 58.4%; Score 686.6; DB 6; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 2e-183;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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VERSION BD015847.1 GI:22556984  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1173)  
AUTHORS Peter, B. and Olaylee, M.A.  
TITLE Novel polypeptide  
JOURNAL Patent: JP 2001211889-A 1 07-AUG-2001;  
PFIZER INC  
COMMENT OS Homo sapiens (human)  
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ED 07-AUG-2001  
PF 27-OCT-2000 JP 2000329359  
PR 29-OCT-1999 GB 9925641:4, 20-APR-2000 GB 0009973:9 PI  
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 VERSION AF329449.1 GI:13876643  
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 AUTHORS Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A.,  
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Gustafson, E.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M.  
 and Monsma, F.J. Jr.  
 Cloning and characterization of a novel human histamine receptor  
 J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)  
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 AUTHORS Monsma, F.J. Jr., Wang, S., Behan, J., Laz, T.M., Greene, J. and  
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Query Match 58.4%; Score 686.6; DB 9; Length 1173;  
 Best Local Similarity 75.1%; Pred. No. 2e-183;  
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
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Db	301	TCGTATATAACATTTGCTCATCAGCTATGATCGATACCTGTCAGTCTCAATGCTGTG	360
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Db	421	GTGCTGGCTTCTTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTTGGAAGGA	476
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QY	661	ACCTCTTCCAGTGTCTCAGGACACTTACAGAGCTGGGGTGGCTTCAGGACACAGTAAT	720
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LOCUS	AY008280	1173 bp	linear
DEFINITION	Homo sapiens histamine receptor H4 (H4) mRNA, complete cds.		
ACCESSION	AY008280		
VERSION	AY008280.1 GI:15822540		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1173)		
AUTHORS	Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and O'Dowd, B.F.		
TITLE	Discovery of H4, a Novel Histamine Receptor		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1173)		
AUTHORS	Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and O'Dowd, B.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-SEP-2000) Pharmacology, University of Toronto, 8 Taddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada		
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RESULT 12
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LOCUS      Homo sapiens histamine receptor H4 (HRH4) mRNA, complete cds.
DEFINITION
ACCESSION      AY136745
VERSION      AY136745.1 GI:22658472
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Publ.H.L. Iii, Ikeda, S.R. and Aronstam, R.S.
Direct Submission
Submitted (26-JUL-2002) cDNA Resource Center, Guthrie Research
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Query Match      58.4%; Score 686.6; DB 9; Length 1173;
Best local Similarity 75.1%; Pred. No. 2e-183;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
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RESULT 13  
LOCUS HSA298292 1173 bp mRNA linear PRI 12-JAN-2002  
DEFINITION Homo sapiens mRNA for histamine receptor H4 (HRH4 gene).  
ACCESSION AJ298292  
VERSION AJ298292.1 GI:18152452  
KEYWORDS histamine receptor H4; HRH4 gene.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS O'Reilly,M.A.  
TITLE Identification of a histamine H4 receptor on human eosinophils -  
Role in eosinophil chemotaxis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1173)  
AUTHORS O'Reilly,M.A.  
TITLE Direct Submission  
JOURNAL Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer  
Ltd, Ramsgate Road, Sandwich, Kent, CT13 9NU, UNITED KINGDOM

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## ORIGIN

Query Match 58.4%; Score 686.6; DB 9; Length 1173;  
Best local Similarity 75.1%; Pred. No. 2e-183;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
QY 1 ATGTCGAGTCTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCTTGGCAATT 60  
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LOCUS  
DEFINITION

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ACCESSION AX376577
VERSION AX376577.1 GI:19170678
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
  1. Lin, D.C., Zhao, J., Chen, J.L. and Cutler, G.
  Novel receptors
  TITLE Patent: WO 0200719-A 5 03-JAN-2002;
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ORIGIN
  Query Match 58.4%; Score 686.6; DB 6; Length 1266;
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  Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
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ACCESSION AX301229
VERSION AX301229.1 GI:17382320
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1. Lind, P., Sejlitz, T., Vogeli, G. and Wood, L.S.
  G protein-coupled receptors
  TITLE Patent: WO 0185793-A 1 15-NOV-2001;
  JOURNAL PHARMACIA & UPJOHN COMPANY (US)
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  Best Local Similarity 75.1%; Pred. No. 2e-183;
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GenCore version 5.1.6  
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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

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Listing first 45 summaries

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9: geneseqn2003cs.\*

10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	958.4	81.5	1176	6	AAI70982 Rat hist
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4	686.6	58.4	1173	3	Aad01124 Human orp
5	686.6	58.4	1173	4	Aaf83203 Human GPC
6	686.6	58.4	1173	5	Aab24007 Human G p
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8	686.6	58.4	1173	6	Abq78739 Nucleotid
9	686.6	58.4	1173	6	AAI70980 Human his
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17	685	58.2	1227	6	AAI66009 Human GPR
18	685	58.2	1265	8	AAI66078 Human DNA
19	685	58.2	1265	8	AAd55125 Human H4
20	683.4	58.1	1173	6	AAI67750 Human his
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## ALIGNMENTS

### RESULT 1

AAI70981 ID AAI70981 standard; cdna; 1176 BP.

XX XX AAI70981;

XX XX AAI70981;

DT 18-MAR-2002 (first entry)

XX XX Mouse histamine H4 receptor cDNA.

XX XX Histamine H4 receptor; mouse; antiallergic;

XX XX antiinflammatory; cardiant; circulatory; antidiabetic; laxative;

XX XX diagnosis; gene therapy; ss.

XX XX Mus musculus.

XX XX W0200192485-A1.

XX XX 06-DEC-2001.

XX XX 22-FEB-2001; 2001WO-US005914.

XX XX 31-MAY-2000; 2000US-0208260P.

XX XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX XX Lovenberg T, Liu C;

XX XX WPI; 2002-114339/15.

XX XX P-PSDB; AAM50565.

XX XX New mammalian histamine H4 receptor proteins and polynucleotides encoding

XX XX the proteins, useful in gene therapy for treating diseases where it is

XX XX beneficial to elevate mammalian histamine H4 receptor activity.

XX XX Claim 4; Fig 5A; 92pp; English.

XX XX The present sequence is that of a cdna clone encoding a murine histamine

XX XX receptor of the H4 subtype. The cdna was isolated from a mouse spleen

XX XX cdna library. It shows 72.8% homology to the human H4 receptor coding

XX XX region. The invention provides mammalian (human, mouse, rat and guinea

XX XX pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and

XX XX polypeptides (see AAM50564-67). The nucleic acids have been expressed in

XX XX recombinant host cells that produce active recombinant protein. The

XX XX pharmacology of known histamine ligands is demonstrated. Mammalian

XX XX histamine H4 receptor may be used in gene therapy for the treatment of

Aad37667 Human G-p  
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Aaa70640 Rat G-pro  
Aal59979 Human H3  
Aal59985 Human H3  
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Aah44575 Rat musca  
Aaa70638 Rat G-pro  
Aht42301 Toxicity  
Aax59168 Rat G pro  
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34 143.2 12.2 1953 3 AAA70638  
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43 140.4 11.9 1334 2 AAH44573  
44 140.4 11.9 1335 2 AAX02886  
45 140.4 11.9 1335 3 AAA09062

CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, treating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity  
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 DT 18-MAR-2002 (first entry)  
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 XX  
 KW Histamine H4 receptor; rat; antiasthmatic; antiallergenic;  
 KW antinflammatory; cardiant; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy; ss.  
 XX  
 OS Rattus rattus.  
 XX  
 PN WO200192485-A1.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 22-FEB-2001; 2001WO-US005914.  
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 PR 31-MAY-2000; 2000US-0208260P.  
 XX  
 PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
 XX  
 PI Lovenberg T, Liu C;  
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 WPI: 2002-114339/15.  
 DR P-PSDB; AAM50566.  
 XX

New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.

Claim 4; Fig 5C; 92pp; English.

The present sequence is that of a cDNA clone encoding a rat histamine receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA library. It shows 72.5% homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the mammalian histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin



XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;  
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;  
XX WPI; 2000-317986/27.  
DR P-PSDB; AAB02831.  
XX Non-endogenous, human G protein-coupled receptors for screening receptor,  
PT inverse or partial agonists useful as therapeutic agents.  
XX Example 1; Page 88-89; 187pp; English.  
XX The present invention describes transmembrane receptors, preferably human  
CC G protein coupled receptors (GPCR), for which the endogenous ligand is  
CC unknown (orphan GPCR receptors). More specifically the present invention  
CC relates to non-endogenous, constitutively activated versions of a human  
CC GPCR. These non-endogenous human GPCRs can be useful for the direct  
CC identification of candidate compounds as receptors agonists, inverse  
CC agonists or partial agonists for use as pharmaceutical agents. ABA46017  
CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
Query Match 58.4%; Score 686.6; DB 3; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 2.4e-204;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
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DB 241 GAATTTGGAGGAATCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGGCCGCA 300  
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DB 715 TCTGCATCGACAGAAAGTTCTCTGCATCTCTTCAATTCAGAGAGACAGAGGAGAAAGAGTAGT 774  
QY 781 ATCTGGTGTCTTAAAGGACTCACATGAACAGCAGTATCAGCTGCTTCAAACTGGGTTCC 840  
DB 775 CTATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTCC 834  
QY 841 TTTGGCGATCGAAAGTGCAGCGCTTCGCAAGGGAGTAGCGAGAGCTTCTCAGAGGC 900  
DB 835 TTTCTCCCAATCAGATTTCTGTAGCTCTTCCACAAAGGGAACATGTTGAATGCTTAGAGGC 894  
QY 901 AGGAGCTAGCCAGCTCACTGGCCATCTTCTGAGCGCTTTTGCATTTGCTGGGCTCCA 960  
DB 895 AGGAGATTAGCAAGTCACTGCGCAATCTCTTAGGGGTTTTTGTGTTTGGGCTCCA 954  
QY 961 TACTGTCTGTTCACAATTTGCTCTTCAACTTACCCAGAAAGGAGCGCCCAAAATCGGTG 1020  
DB 955 TATTCCTCTGTTCACAATTTGCTCTTCAATTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014  
QY 1021 TGGTACAGATTTGCTTCTGCTGCAATGCTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080  
DB 1015 TGGTATAGAAATGCAATTTTGGCTTCAAGTGGTTCAATTCCTTGTCAATCTCTTTTGTAT 1074  
QY 1081 CCTTGTCTCAGAGCGTTTCCAGAGGCTTCTGGAAGATCTTGTGTGACAAAGCAA 1140  
DB 1075 CCATTTGTCTCAGAGCGTTTCCAAAGGCTTCTTGAATAATTTTGTATAAAAAGCAA 1134  
QY 1141 CCAGCGCTGTCCACAGAAC---CAGTCAGTATCTTCTTGA 1176  
DB 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCTTAA 1173  
RESULT 4  
AAB01124  
ID AAB01124 standard; cDNA; 1173 BP.  
XX  
AC AAB01124;  
XX  
DT 02-NOV-2000 (first entry)  
XX Human orphan G protein-coupled receptor hrUP7 cDNA.  
DE Human; orphan G protein-coupled receptor; GPCR; hrUP7; drug screening;  
KW transmembrane receptor; signal cascade; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1..1173  
FT /\*tag= a  
FT /product= "hrUP7"  
FT /note= "Human orphan G protein-coupled receptor"  
XX  
PN WO2000031258-A2.  
XX  
PD 02-JUN-2000.  
XX  
PF 13-OCT-1999; 99WO-US023687.  
XX  
PR 20-NOV-1998; 98US-0109213P.  
PR 16-FEB-1999; 99US-0120416P.  
PR 26-FEB-1999; 99US-0121852P.  
PR 12-MAR-1999; 99US-0123946P.  
PR 12-MAR-1999; 99US-0123949P.  
PR 28-MAY-1999; 99US-0136436P.  
PR 28-MAY-1999; 99US-0136437P.  
PR 28-MAY-1999; 99US-0136439P.  
PR 28-MAY-1999; 99US-0136567P.  
PR 28-MAY-1999; 99US-0137127P.

PR 28-MAY-1999; 99US-0137131P.  
 PR 29-JUN-1999; 99US-0141448P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156633P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 29-SEP-1999; 99US-0156653P.  
 PR 01-OCT-1999; 99US-0157280P.  
 PR 01-OCT-1999; 99US-0157281P.  
 PR 01-OCT-1999; 99US-0157282P.  
 PR 01-OCT-1999; 99US-0157293P.  
 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 PR 12-OCT-1999; 99US-00417044.  
 XX (AREN-) ARENA PHARM INC.  
 XX  
 XX Chen R, Dang HT, Liaw CW, Lin I;  
 XX  
 XX WPI; 2000-400068/34.  
 DR P-PSDB; AAY71297.  
 XX  
 PT Novel human orphan G protein-coupled receptors and the encoding cDNAs for  
 PT use in the identification of G protein-coupled receptor agonists.  
 XX  
 PS Claim 25; Page 59; 102pp; English.  
 XX  
 CC The present sequence is a cDNA encoding hrup7, an endogenous human orphan  
 CC G protein-coupled receptor (GPCR). The full length hrup7 cDNA was cloned  
 CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan  
 CC GPCR of the invention, like all GPCRs has seven transmembrane alpha  
 CC helices with an extracellular N-terminus and an intracellular C-terminus.  
 CC However, no endogenous ligands has yet been identified for the proteins  
 CC of the invention. The orphan GPCRs may be used in the identification of  
 CC their endogenous ligands, and to screen potential GPCR agonists and  
 CC antagonists for use as pharmaceutical agents. The proteins may also be  
 CC used in the study of GPCR-mediated signalling cascades, and to elucidate  
 CC their precise role in normal and diseased human conditions. Nucleic acid  
 CC encoding human orphan GPCRs may be used for tissue localisation  
 CC expression analysis to provide information about their function in  
 CC healthy and pathological states  
 CC  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 3; Length 1173;  
 Best Local Similarity 75.1%; Pred. No. 2.4e-204;  
 Matches 88; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTGGAGTCTAACAGTACTGGCATCTGCCACCAGCTGCTCAGGTCCTTGGCATTT 60  
 DB 1 ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
 QY 61 TTAATGCTTCATTTGCTTGTCTATTAATGTTAGGCAATGCTGGTCACTTTAGCCTTT 120  
 DB 61 TTTATGCTCTTAGTGTCTTTGTCTATTAATGCTAGGAAATGCTTTGGTCACTTTAGCCTTTT 120  
 QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180  
 DB 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCACTCT 180  
 QY 181 GACTTCTCTGGTGTGATCTCAATTCCTCTGTACATCCCTCACGCTGTTTGAATGG 240  
 DB 181 GACTTCTCTGGTGTGATCTCAATTCCTCTGTACATCCCTCACGCTGTTTGAATGG 240  
 QY 241 AATTGGAAGTGAATCTGCATGTTTGGCTCACTACTGACTATCTTTGTGTCACCGCA 300  
 DB 241 GATTTTGGAAAGAAATCTGTGATTTTGGCTCACTACTGACTATCTTTGTATGTACGCA 300  
 QY 301 TCTGTCTACAAATATGTCCTCATTAGCTAGCATGATACAGTACAGTTCAGTTCATGCTGTG 360  
 DB 301 TCTGTATATTAACATGTGCTTCATCAGCTATGATGATGATGATGATGATGATGATGATG 360  
 QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTTTTGG 420

Db 361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGTTGGCCGTTTGG 420  
 QY 421 ATACTGGCTTTCTTGGTAATGSCCGCATGATTTCTGCTTCAGATTCTTGGAAAGAACAGC 480  
 Db 421 GTCTGGCCCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGGGAAGGA 476  
 QY 481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTTACAGAGTGGTACATCTCTCACCATTACA 540  
 Db 477 --TGAAGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTCTTGGCATCACA 534  
 QY 541 ATGCTCTTGAATTCCTGCTTCTCTGTCATCTCTGTGGCTTTATTTCAATGTACAGATTAC 600  
 Db 535 TCATTCTTGGAAATTCGTGATCCAGTCATCTTAGTGGCTTTATTTCAACATGAATATTAT 594  
 QY 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGTGGCCCTAGCCATGTCGATTTCTCCTACT 660  
 Db 595 TGGAGCCTGTGGAAGCGTAGTATCTCAGTAGTGGCCAAAGCCATCCTGGAGTACTGCT 654  
 QY 661 ACCTCTTCCAGTCTTCAGGACACTTACACAGAGCTGGGGTGGCTTTCAGGACACAAAGTAAT 720  
 Db 655 GTCTCTCCAACTCTGTGGACACTATTCCAGAGTAGACTATCTTCAAGGAGATCTCTT 714  
 QY 721 CCTGGATTGAAGAAATCAGCTGCATCTCGTCACTCAGAAAAGTCTCTCGAAGAAAGAGCAGC 780  
 Db 715 TCTGCATCGACAGAGTTCCTGTCATCTTCAATTCAGAGACAGAGAGGAGAGTAGT 774  
 QY 781 ATCTGTGTCTTTAAGGACTCATGAACAGCAGATATCACTGCCTTCAAAGTGGGTTC 840  
 Db 775 CTCATGTTTTCTTCAAGAACCAAGATGAATAGCAATAAATGCTTCCAAAATGGGTTC 834  
 QY 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAAGGGAGTACGACAGCTTCTCAGAGGC 900  
 Db 835 TTCTCCCAATCAGATCTGTAGCTCTTCCAAAGGGAGACATGTTGACCTTTAGAGCC 894  
 QY 901 AGAAGCTAGCCAGTCACTGGCCATCTTCTCAGAGCGCTTTTCCCATTTCTGGGCTCCA 960  
 Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTGTTCTGGGCTCCA 954  
 QY 961 TACTGTCTGTTCACAAATGTCCTTTCACTTACCAGAGCGGAACGCCCAATCGGTG 1020  
 Db 955 TATTCTGTCTCAAAATGTCCTTTCAATTTATTTCTCAGCAACAGGTCCTCAATCAGTT 1014  
 QY 1021 TGTGTACAGCATTCCTTCTGGCTGCAATGTTCAATTTCTGTTTAAATCCCTTTCTGTAC 1080  
 Db 1015 TGTGTATAGATTCATTTTGGCTCAGTGTGTTCAATTTCTTGTCAATCTCTTTTGTAT 1074  
 QY 1081 CCTTTGTGTACAGGCGTTTCCAGAAAGGCTTTCTGGAAGATACCTTTGTGTCACAAAGCAA 1140  
 Db 1075 CCATTGTGTACAGGCGTTTCCAAAGGCTTTCTTGAATAATTTTGTATAAAAAAGCAA 1134  
 QY 1141 CCAGCGCTGTACAGAAC---CAGTCAATATCTTTTGA 1176  
 Db 1135 CCTCTACCATCAACACAGCTCGGTCAATCTTCTTAA 1173

## RESULT 5

AAF83203

ID AAF83203 standard; cDNA; 1173 BP.

XX AAF83203;

AC AAF83203;

XX AAF83203;

DT 09-JUL-2001 (first entry)

XX

DE Human GPCR-like polypeptide, PFI-013 encoding cDNA.

XX

XX

KW G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;

KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;

KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;

XX signal transduction; ss.

OS Homo sapiens.

XX

FH Key

Location/Qualifiers

FT	1. .1173	
FT	/*tag= a	
FT	/product= "PFI-013"	
XX		
PN	EPI096009-A1.	
XX		
PD	02-MAY-2001.	
XX		
XX	24-OCT-2000; 2000EP-00309364.	
XX		
PR	29-OCT-1999; 99GB-00025641.	
PR	20-APR-2000; 2000GB-00009973.	
XX		
XX	(PFIZ ) PFIZER LTD.	
PA	(PFIZ ) PFIZER INC.	
XX		
XX	Peter B, O'reilly MA;	
XX		
XX	WPI; 2001-309854/33.	
DR	P-PSDB; AAB62445.	
XX		
PT	New G-protein coupled receptor-like polypeptide, polynucleotide for	
PT	screening drug candidates for treating diseases associated with signal	
PT	transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.	
XX		
PS	Claim 1; Page 43; 66pp; English.	
XX		
CC	This cDNA of NCMB 41073 encodes a human G-protein coupled receptor	
CC	(GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be	
CC	expressed by standard recombinant methodology. Antibodies and modulators	
CC	of PFI-013 are useful in the manufacture of a medicament for treating	
CC	allergic disorder, including extrinsic asthma, immunological disorders,	
CC	such as intrinsic asthma, vasculitic granulomatous disease, interstitial	
CC	and other pulmonary disease, including chronic obstructive pulmonary	
CC	disease (COPD), infectious, inflammatory disease, such as inflammatory	
CC	bowel disease and neoplastic and myeloproliferative diseases. They are	
CC	also useful for treating obesity, diabetes, metabolic, neurological	
CC	diseases, psychotherapeutics, urogenital disease, reproduction and sexual	
CC	medicine, inflammation, cancer, tissue repair, dermatology, photoageing,	
CC	skin pigmentation, osteoporosis, cardiovascular, gastrointestinal	
CC	diseases, allergy and respiratory disease, sensory organ disorders, sleep	
CC	disorders and hair loss. The PFI-013 protein and nucleic acid are useful	
CC	in the diagnosis and treatment of the above conditions and also for	
CC	screening drug candidates for the treatment of diseases associated with	
CC	signal transduction. The antibodies are also useful for enrichment of	
CC	eosinophils from mammalian, especially human blood and for detecting the	
CC	protein in biological samples	
XX		
SQ	Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;	
	Query Match 58.4%; Score 686.6; DB 4; Length 1173;	
	Best Local Similarity 75.1%; Fred. No. 2.4e-204;	
	Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2	
Qy	1 ATGTCGAGTCTAACAGTACTGGCATTCTGGCCACAGCTGTCAGTCCCTTGGCATT 60	
Db	1 ATGCCAGATACATAATAGCACAAATCAATTATCATAAGCACTCGTGTACTTTAGCATTT 60	
Qy	61 TTAATGCTTCATTGGCTTTGGCTATATATGGTAGGCAATGCTGGTCAATCTTAGCCTTT 120	
Db	61 TTTATGTCCTTAGTAGCTTTTGGCTATATATGCTAGGAATGCTTTGGTCATTTTAGCTTTT 120	
Qy	121 GTGTGGACAGAAACCTTAGACATCGAAGTAAATTAATTTTTTCTTAATTTGGCTATTTCT 180	
Db	121 GTGTGGACAAAAACCTTAGACATCGAAGTAGTATATTTTTTCTTAACCTGGCCATCTCT 180	
Qy	181 GACTTTCCTCGTGGTTCATTTCCATTCCTCTGTATACATCCCTCACGTTGTTTAACTGG 240	
Db	181 GACTTCTTTGGGTGGTGATCTCCATTCTTTGATACATCCCTCACAGCTGTTGGAATGG 240	
Qy	241 AATTTGGAAGTGAATCTGCATGTTTGGCTCAATTAATGACTATCTTTTGTGCACCGCA 300	
Db	241 GATTTTGCAAAGGAATCTGTGTAATTTTGGCTCACTACTGACTACTGTATATGTACAGCA 300	



histamine H3 receptor homologue; infection; viral; bacterial; fungal;  
 protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;  
 bulimia; osteoporosis; asthma; allergy; urinary retention;  
 acute heart failure; hypotension; hypertension; angina pectoris;  
 myocardial infarction; stroke; ulcer; migraine; vomiting;  
 psychotic disorder; neurological disorder; anxiety; schizophrenia;  
 manic depression; bipolar disorder; depression; delirium; dementia;  
 severe mental retardation; dyskinesia; Parkinson's disease;  
 Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;  
 macrophage; eosinophil; neutrophil; function modulation;  
 autoimmune disorder; pulmonary disorder; gene therapy; vaccine;  
 drug screening; signal transduction; transgenic animal; drug discovery;  
 ss.

XX Homo sapiens.

Key Location/Qualifiers  
 CDS 1..1173  
 /tag= a  
 /product= "Human AXOR35"  
 /note= "G protein-coupled receptor"

WO200133221-A1.

XX 10-MAY-2001.

XX 26-OCT-2000; 2000WO-US029461.

XX 02-NOV-1999; 99US-00431898.

PR 03-FEB-2000; 2000US-00497790.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;

PI Michalovich D, Morrow DM, Zhu Y;

XX WPI: 2001-316464/33.

DR P-PSDB; AAB73622.

Novel G-protein coupled receptor polypeptide and polynucleotide for treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma.

Claim 2; Page 49-50; 54pp; English.

The invention relates to the human G protein-coupled receptor AXOR35 (AAB73621), to cDNA encoding AXOR35 (AAB74006), and to AXOR35 fragments and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative transmembrane domains and is involved in signal transduction. AXOR35 has homology and structural similarity with G protein-coupled receptors such as the human histamine H3 receptor. The invention also relates to expression vectors and host cells comprising AXOR35 DNA, to recombinant expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins and nucleotides may be used to treat a wide variety of disorders including bacterial, fungal, protozoal and viral infections, particularly HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy; diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting; psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental retardation, and dyskinesias, such as Parkinson's disease, Huntington's disease or Gilles de la Tourette's syndrome. AXOR35 proteins and nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and antibodies may be used in screening compounds for their ability to modulate AXOR35 activity or expression. Such AXOR35 modulators are particularly useful for treating asthma, and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils or neutrophils in asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also useful for diagnosing or determining susceptibility of an individual to a disease via the detection of abnormal levels of protein or mRNA, or via the detection of mutations in the corresponding gene. AXOR35 proteins are

CC also useful for inducing an immunological response in a mammal against  
 CC the above diseases, and for antibody production. AXOR35 nucleotides are  
 CC also useful as diagnostic reagents, in chromosome localisation and tissue  
 CC expression studies, and for producing transgenic animals useful in drug  
 CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35  
 CC protein or fragments thereof, and are also useful for treating conditions  
 CC associated with the expression of the AXOR35 protein. The present  
 CC sequence represents cDNA encoding human AXOR35

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

SQ Query Match 58.4%; Score 686.6; DB 5; Length 1173;

Best Local Similarity 75.1%; Pred. No. 2.4e-204;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACAGTACTGGGATCTTGGCCACAGCTGCTCAGGTCCCTTGGCAATTT 60

DB 1 ATGCCAGATCTACTAATAGCACCAATCAATTTATCATCAAGCACTCGTGTACTTTAGCAATTT 60

QY 61 TTAATGTCCTTCATTTGGCTTTGCTATATAATGTTAGGCAATGCTGTGTCATCTTAGCCTTT 120

DB 61 TTTATGTCCTTAGTAGCTTTTGTCTATATAGCTAGGAATGCTTTGTGTCATTTTAGCTTTT 120

QY 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180

DB 121 GTGTGGACAGAAACCTTAGACATCGAAGTAGTATTTTTTCTTAACCTTGCCCATCTCT 180

QY 181 GACTTCTCGTGGGTTTGATTTCCATTTCTGTACATCCCTCAGCTGTGTTAACTGG 240

DB 181 GACTTCTTTTGGGTGTGATCTCCATTCCTTTGTATCCTCCACACGCTGTTCGAATGG 240

QY 241 AATTTTGAAGTGAATCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCAACGCA 300

DB 241 GAATTTGGAAGGAATCTGTGTATTTTGGCTCCTACTGACTATCTGTTATGTACAGCA 300

QY 301 TCTGTCTACAATATTGCTCTCATTTAGCTACGATCGATACCACTCAGTTTCAATGCTGTG 360

DB 301 TCTGTATATACATTTGCTCTCATCAGCTATGATCGATACCTGTCAGTCTCAATGCTGTG 360

QY 361 TCTTATAGGCTCAACACACTGGGATCATGAGAGATGTTTGTCAATAGTGTGCTGTTGG 420

DB 361 TCTTATAGAACTCAACATACTGGGCTCTTGAAGATTGTTACTCTGATGTTGGCCGTTGG 420

QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATCTTGGCTTCAGATTCTTGGAGACAGC 480

DB 421 GTGCTGGCTTCTTAGTGAATGGGCAATGATCTAGTTTCAGAGTCTTTGGAAGGA --- 476

QY 481 ACGAACACAAAGGACTGTGAGCTGGCTTTTGTGTACAGAGTGTGTACATCCTCAACATTACA 540

DB 477 --TGAAGGTAGTGAATGTGAACCTGGAATTTTTCGGAATGTTACATCCTTCCCATCACA 534

QY 541 ATGCTCTTGGAAATTCCTGCTTCTGTCTATCTGTGGCTTATTTCAATGTACAGATTTCAC 600

DB 535 TCATCTTTTGGAAATTCGTGATCCAGTCACTCTTAGTGGCTTATTTCAACATGAATATTTAT 594

QY 601 TGGAGCTGTGGAAGCGTAGGCTCTCAGTAGTGCCCTAGCCATGCTGGATTTCTCCACT 660

DB 595 TGGAGCTGTGGAAGCGTAGTCACTCTCAGTAGTGCCAAAGCCATCCTGGACTGATGCT 654

QY 661 ACCTCTTCCAGTCTTCAGGACACTTTACAGAGCTGGGGTGGCTTTCAGAGGACCAAGTAAT 720

DB 655 GTCTCTTCCAACATCTGTGGACACTCATTTACAGAGTAGACTATCTTCAAGGAGATCTCTT 714

QY 721 CTGGAATGAAGGAATCAGTCTGATCTCGTCTACTCAGAAAGTCTTCGAAAGAAAGAGCAGC 780

DB 715 TCTGCAATCGACAGAAGTTCCTGCATCTCTTTCATTTCAGAGACAGAGAGAGAGAGTAGT 774

QY 781 ATCTGCTGTCTTGAAGACTTCAGATGACACAGATATCACTGCTCTCAAGTGGGTTCC 840

DB 775 CTCATGTTTCTTCAAGAACCAAGATGAATAGCAATATCAATTTGCTTCCAAAATGGGTTCC 834

QY 841 TTTCTGCGCATCGAAAGTGCAGCGCTTCGCCAAAGGAGTAGTCAGAGAGCTTCTTCAGAGCG 900

Db 835 TTCTCCCAATCAGATCTCTAGCTCTTTCACAAAGGGAACATGTTGAACCTCTTAGAGCC 894  
 QY 901 AGGAAGCTAGCCAGCTCACTGGCCATCTCTGAGCGCTTTTGCCATTTGCTGGCTCCA 960  
 Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTGAGCGCTTTTGCTGGCTCCA 954  
 QY 961 TACTGTCTGTTTCAAAATGCTCTTCAACTTTACCCAGAACGGAACGCCCAAAATCGGTG 1020  
 Db 955 TATCTCTGTTTCAAAATGCTCTTCAACTTTACCCAGAACGGAACGCCCAAAATCGGTG 1014  
 QY 1021 TGGTACAGCATGCTCTGCTGCAATGCTTCAATTTGCTGGCTCCA 1080  
 Db 1015 TGGTATGAATGCAATTTGGCTTCAAGTCTGCTGCTTCAATTTGCTGGCTCCA 1074  
 QY 1081 CCTTTGTTGTCACAGCGCTTTCCAGAGGCTTTCTGGAAGATACCTTTGCTGCAAGACAA 1140  
 Db 1075 CCATTTGTTGTCACAGCGCTTTCCAGAGGCTTTCTGGAAGATACCTTTGCTGCAAGACAA 1134  
 QY 1141 CCAGCGGTGTCACAGAAC--CAGTCAAGTACCTTTGGA 1176  
 Db 1135 CCTCTACCATCACACACAGTCGGTCAAGTATCTTTAA 1173

RESULT 7

ABZ80663  
 ID ABZ80663 standard; cDNA; 1173 BP.

AC ABZ80663;

DT 13-JUN-2003 (first entry)

DE Human histamine receptor coding sequence.

KW human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;  
 KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;  
 KW anti-migraine; cardiant; anti-rheumatic; anti-arthritis; antipsoriatic;  
 KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;  
 KW myocardial infarction; migraine; chronic obstructive pulmonary disease;  
 KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;  
 KW psoriasis; receptor.

XX Homo sapiens.

OS  
 FH Key Location/Qualifiers  
 CDS 1..1173  
 FT /\*tag= a  
 FT /product= "Histamine receptor"

XX US6204017-B1.

XX 20-MAR-2001.

XX 07-OCT-1999; 99US-00414010.

XX 07-OCT-1999; 99US-00414010.

XX (SCHE ) SCHERING CORP.

XX Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;  
 PI Wang S;

XX WPI; 2002-442063/47.

DR P-PSDB; ABO98629.

XX New nucleic acid encoding antigenic part of human histamine receptor,  
 PT useful for preparing antibodies, e.g. for treating-histamine related  
 PT disorders.

XX Example 1; Col 27-28; 19pp; English.

XX This sequence represents the open reading frame for a human histamine  
 CC receptor (HR) designated SP9144. The sequence was isolated by searching  
 CC databases with the sequence of known G-coupled protein receptor (GPCR).

CC The gene is used for recombinant production of HR and for preparing  
 CC antibodies (Ab). These Ab are used to purify HR by immunoaffinity  
 CC chromatography, in immunoassay of histamine receptor, to identify cDNA  
 CC clones that express the receptor, as antagonist to block binding of  
 CC histamine (for treating any histamine-associated disorder) and to  
 CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR  
 CC protein can be used in the treatment of e.g. inflammation, asthma,  
 CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,  
 CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple  
 CC sclerosis, inflammatory bowel disease and psoriasis

XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 6; Length 1173;  
 Best Local Similarity 75.18; Pred. No. 2.4e-204;  
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
 QY 1 ATGTCGGAGTCTAAGTACTGGCATCTGCGCCAGCTGCTCAGGTCCCTTGGCATTT 60  
 Db 1 ATGCCAGATACATAAGACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
 QY 61 TTAATGCTTCATTTGCTTTGCTATATGCTAGCAATGCTGTGGTTCATCTTAGCCTTT 120  
 Db 61 TTAATGCTTCATTTGCTTTGCTATATGCTAGCAATGCTGTGGTTCATCTTAGCCTTT 120  
 QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTTCT 180  
 Db 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTTCT 180  
 QY 181 GACTTCCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240  
 Db 181 GACTTCCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240  
 QY 241 AATTTTGGAGTGAATCTGCACTGTTTGGCTACTTACTGACTATCTTTGTCACCGCA 300  
 Db 241 GATTTTGGAGGAAATCTGTGTAATTTGGCTACTTACTGACTATCTTTGTCACCGCA 300  
 QY 301 TCTGCTACAAATATGTCCTCATTAGCTACGATCGATACCACTCAGTTCAGTTTCAATGCTGTG 360  
 Db 301 TCTGCTATATAACATTTGCTCCTCATCAGCTATGATCGATACCTGTCAGTCTCAATGCTGTG 360  
 QY 361 TCTTATAGGGCTCAACACACTGGGCATCATGAAGTAATTTGTTGCTCAAAATGGTGGCTTTGG 420  
 Db 361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCGCTTTGG 420  
 QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATCTGCTTCAGATTTCTTGAAGAACAGC 480  
 Db 421 GTGCTGGCTTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGAAGAAC 476  
 QY 481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCTCCATTCACA 540  
 Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAAATGGTACATCTTGGCCATCACA 534  
 QY 541 ATGCTCTTGGAAATTCCTGCTTCTGCTCATCTCTGCTGCTATTTCAATGACATTTAC 600  
 Db 535 TCATTCTTGGAAATTCGTTGCTCCAGTCTATCTTAGTCTGCTATTTTCAACATGAATTTAT 594  
 QY 601 TGGAGCTGTGGAAGCGTGGGCTCTCAGTAGGTGCTCCCTAGCCATGCTGGATTCTCCACT 660  
 Db 595 TGGAGCTGTGGAAGCGTGGTATCTATCTAGTAGGTGCTCCAAAGCCATCTTGGACTGCT 654  
 QY 661 ACCTCTTCCAGTGTCTTCCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720  
 Db 655 GTCTCTTCCAAACATCTCTGGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
 QY 721 CCTGGATTGAAGGAATCAGCTGATCTCGTCACTCAGAAAGTCTCCGAAAGAGAGCAGC 780  
 Db 715 TCTGCATCGACAGAAAGTTCCGCAATCTTCAATTCAGAGAGACAGAGAGAGAGTAGT 774  
 QY 781 ATCTGCTGTCTTAAAGGACTCACATGAACAGCAGTATCACTGCTTCAAGTGGGTTC 840  
 Db 775 CTCAATGTTTCTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGGTTC 834



Db	715	TTCTG	CATC	GACG	AGAGTT	CTCTG	CATC	CTTTCA	TTCA	GAGAC	CAGAG	GAGAA	GAGTAG	774
Qy	781	ATCCT	GGTCT	CTTA	AGGACT	CA	CATGA	ACAG	CAGAT	CAC	TGCCT	TTCA	AGTGG	840
Db	775	CTCAT	TTTTCT	CTCA	AGAAC	CAAGAT	GAATAG	CAATAC	CAAT	TGCTT	CTCA	AAATGG	834	
Qy	841	TTCTG	CGCAT	CGGAA	AGTGC	AGCGCT	TCG	CCAA	GGGAGT	ACG	CAGAG	CTTCT	CAGAGC	900
Db	835	TTCTC	CCAAT	CAGAT	TCTGT	AGTCTT	CAC	CAAG	GGACAT	TGTTG	AACTG	CTTAGAGC	894	
Qy	901	AGGA	GCTAG	CCAGG	TCAC	TGGCCAT	CCCTT	CTG	AGCGCT	TTT	TGCCA	TTTGT	CGGGCTCA	960
Db	895	AGGAG	ATTAG	CCAAGT	CAC	TGGCCAT	CTCT	CTT	AGGGGT	TTTT	TGCTG	TTGCT	GGGCTCA	954
Qy	961	TACTG	TCTG	TTACA	ATTG	TCCCTT	CAACT	TAC	CCCA	AGGAA	CGCCCA	CAATCG	GTG	1020
Db	955	TATTCT	CTGT	CAAA	TTG	TCCCTT	CATT	TTAT	TCCT	CAGCA	CAGCT	CTTAAT	CAGTT	1014
Qy	1021	TGCTAG	CAGCAT	TGCC	TTCT	CGGCTG	CAAT	GTGTT	CAAT	TCGTT	TAAT	CCCTT	CTGTAC	1080
Db	1015	TGGTAT	AGAA	TTGCA	TTT	TGGCTT	CAGT	GGTTCA	ATT	CCCTT	GTG	CAATC	CTCTTT	1074
Qy	1081	CCTTT	GTGT	CAC	AGGCG	TTTT	CCG	AAAG	GGCTTT	CTG	GAAGT	ACTTT	GTGTG	1140
Db	1075	CCATT	GTGT	CAC	AGGCG	TTT	CAAA	AGGCTT	CTT	TGAA	AAATAT	TTTT	GTATA	1134
Qy	1141	CGAG	CGCTGT	CA	GAGAAC	---	CGT	CA	GTAT	CTCT	TTGA			1176
Db	1135	CCCT	CTAC	CAAT	CAAC	ACAC	AGCT	CGGT	CA	GTAT	CTCT	TTAA		1173

## RESULT 9

AAI70980	AAI70980 standard; cDNA; 1173 BP.
XX	
XX	AAI70980;
XX	
XX	18-MAR-2002 (first entry)
XX	
XX	Human histamine H4 receptor cDNA.
XX	
XX	Histamine H4 receptor; human; antiasthmatic; antiallergenic;
KW	antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW	diagnosis; gene therapy; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200192485-A1.
XX	
PD	06-DEC-2001.
XX	
PF	22-FEB-2001; 2001WO-US005914.
XX	
PR	31-MAY-2000; 2000US-0208260P.
XX	
PA	(ORTH ) ORTHO-MCNEIL PHARM INC.
XX	
PI	Lovenberg T, Liu C;
XX	
DR	WPI; 2002-114339/15.
DR	P-PSDB; AAM50564.
XX	
PT	New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT	the proteins, useful in gene therapy for treating diseases where it is
PT	beneficial to elevate mammalian histamine H4 receptor activity.
XX	
PS	Claim 4; Fig 1; 92pp; English.
XX	
CC	The present sequence is that of cDNA clone pH4R encoding a human
CC	histamine receptor of the H4 subtype. The cDNA was isolated from a bone
CC	marrow cDNA library. The invention provides mammalian (human, mouse, rat
CC	and guinea pig) histamine H4 receptor nucleic acid molecules (see



```
Db 421 GTGCTGGCCCTTTAGTGAAGGCGCAATGATTTCTAGTTTCAGAGTCTTGGAAAGA----- 476
Qy 481 ACGAACAACAAGGACTGTGAGCGCTGGCTTTGTTTACAGAGTGGTATCATCTCTCACCATTAACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGGAATGGTATCATCTCTGGCCATCACA 534
Qy 541 ATGCTCTTTGGAATTCCTGCTTCTGCTGTCATCTCTGTGGCTTATTTTCAATGATACAAATTAC 600
Db 535 TCATTCTTTGGAATTCGTGATCCAGTCCATCTTAGTCGCTTATTTCAACATGAATATTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTAGGCTCTCAGTAGTGGCTTACCTAGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 595 TGGAGCCTGTGGAAGCGTAGTATCTCAGTAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654
Qy 661 ACCTCTTCCAGTGTCTCAGGACCTTACAGAGCTGGGCTTGGCTTGGAGACAAAGTAAT 720
Db 655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGATTTGAAGGAATCAGCTGCATCTGCTCACTCAGGAAGTCTCTGGAAGAGAGCAGC 780
Db 715 TCTGATCGACAGAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774
Qy 781 ATCTGTGTGCTTAAAGGACTCAGATGAACAGCAGTATCACTGCTTCAAAAGTGGGTTCC 840
Db 775 CTCAATGTTTCTCAGAACCAAGATGATAGCATACAAATGCTTCCAAATGGGTTCC 834
Qy 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAAGGGAGTACGAGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTTCTGTAGTCTTCCACCAAGGGAACATGTTGAACCTGCTTAGAGCC 894
Qy 901 AGGAAGCTAGCAGGTGCTAGTGGCTTCTGAGCGCTTGTGCAATTTGCTGGGCTCCA 960
Db 895 AGGAATTAGCAAGTCACTGCGCAATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954
Qy 961 TACTGTCTGTTCACAATGCTCTTCACTTACCCAGAGAGCGGCCCAAAATCGGTG 1020
Db 955 TATCTCTGTTCACAATGCTCTTCACTTATCTCAGCAACAGGCTTCAATCAGTT 1014
Qy 1021 TGGTACAGATTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1015 TGGTATAGATTCGATTTTGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
Qy 1081 CCTTTGCTCAGAGCGCTTCCAGAGCGCTTCTGGAAGATCTTGTGTCAGAAAGCAA 1140
Db 1075 CAAATGTGTCAAGCGCTTCCAAAGGCTTCTTGAAGAAATATTTGTATATAAAGCAA 1134
Qy 1141 CCAGCGCTGTCAAGAAC---CAGTCAGTATCTTCTTGA 1176
Db 1135 CCTCTACCATCAACACAGTCGGTCACTATCTTCTTAA 1173
```

## RESULT 11

ACA93262  
ID ACA93262 standard; cDNA; 1173 BP.

XX ACA93262;  
XX AC

XX 16-JUL-2003 (first entry)  
XX

DE Human cDNA encoding GPCR hrup7.  
XX

XX Human; ss; gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;  
KW hARE-5; hrup3; hrup5; hrup6; hrup7; hGPCR27; hARE-1; hARE-2; hPR1; hG2A;  
KW hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hruf4; signalling cascade.  
XX

OS Homo sapiens.  
XX

XX US2003017528-A1.  
PN

XX 23-JAN-2003.  
PD

XX 06-JUN-2001; 2001US-00875076.  
XX PF

XX 20-NOV-1998; 98US-0109213P.  
PR 16-FEB-1999; 99US-0120416P.  
PR 26-FEB-1999; 99US-0121852P.  
PR 12-MAR-1999; 99US-0123946P.  
PR 12-MAR-1999; 99US-0123949P.  
PR 28-MAY-1999; 99US-0136436P.  
PR 28-MAY-1999; 99US-0136437P.  
PR 28-MAY-1999; 99US-0136439P.  
PR 28-MAY-1999; 99US-0136587P.  
PR 28-MAY-1999; 99US-0137127P.  
PR 28-MAY-1999; 99US-0137131P.  
PR 29-JUN-1999; 99US-0141448P.  
PR 28-SEP-1999; 99US-0156333P.  
PR 28-SEP-1999; 99US-0156555P.  
PR 29-SEP-1999; 99US-0156634P.  
PR 12-OCT-1999; 99US-00417044.  
XX

(CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIAN/) LIAN C W.  
PA (LINI/) LIN I.  
XX

Chen R, Dang HT, Liaw CW, Lin I;

WPI; 2003-428952/40.

P-PSDB; ABU92265.

Novel endogenous, orphan, human G protein-coupled receptors useful for identification of modulators of the receptor and as research tools for understanding the role of the receptor in human body.

Claim 25; Page 22; 54pp; English.

The invention relates to a human G protein-coupled receptor (GPCR) appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93258-ACA93274) named hARE-3, hARE-4, hARE-5, hrup3, hrup5, hrup6, hrup7, hGPCR27, hARE-1, hARE-2, hPR1, hG2A, hCHN3, hCHN4, hCHN6, hCHN8, hCHN9, hCHN10 and hruf4. Also included are a plasmid comprising a vector and one of the cDNAs above and a host cell comprising the plasmid. The GPCRs are useful for the direct identification of candidate compounds as inverse agonists, agonists or partial agonists. In vitro and in vivo systems incorporating GPCRs is useful for elucidating and understanding the roles these receptors play in the human condition, both normal and diseased, as well as understanding the role of constitutive activation as it applies to understanding the signalling cascade. The cDNAs are useful for making a probe for dot-blot analysis against tissue mRNA and/or RT-PCR identification of the expression of the receptor in tissue samples. The present sequence is a cDNA encoding a GPCR of the invention

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other; SQ

Query Match 58.4%; Score 686.6; DB 7; Length 1173;

Best Local Similarity 75.1%; Pred. No. 2.4e-204;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACAGTACTGGCATCTTCCACACAGCTGCTCAGTCCCTTGGCATTT 60

Db 1 ATGCAGATACTAATAGCACATCAATTTATCACTAAGCACTCGTTACTTTAGCATTT 60

Qy 61 TTAATGTCTTCATTTGCCCTTTCCTATATATGGTAGCAATGCTGTGGTCACTTAGCCTTT 120

Db 61 TTTATGTCTTATAGTACTTTTGTCTATATGCTAGGAAATGCTTTGGTCATTTTAGCTTT 120

Qy 121 GTGTGGACAGAAACCTTAGACATCGAGTATATTTTCTTAATTTGGCTATTTCT 180

Db 121 GTGTGGACAAACCTTAGACATCGAGTATATTTTCTTAATTTGGCTATTTCT 180

Qy 181 GACTTCTCTGCTGGGTTTGAATTTCCATTCTCTGTACATCCCTCAGCTGTGTTAACTGG 240

Db 181 GACTTCTTGTGGGTGTGATCTCCATCTCTTGTACATCCCTCAGCTGTGTTAACTGG 240

Qy 241 AATTTTGGAAATGGAAATCTGCAATGTTTGGCTACTACTGACTATCTTTTGGCACCGCA 300

Db 241 GATTTCGAAAGGAAATCTGTGTATTTTGGCTCACTACTGCTATCTGTATGTACAGCA 300  
Qy 301 TCTCTCTACAAATATTTCTCATTAGCTACGATCGATACCACTCAGTTTCAAAATGCTGTG 360  
Db 301 TCTGTATATACATTTCTCATCAGCTATGATGATACCTGTCAGTCTCAAAATGCTGTG 360  
Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGCTGTGTTGG 420  
Db 361 TCTTATAGAACTCAACACTCTGGGCTCTGAAGATTGTTACTCTGATGGTGGCCGTTGG 420  
Qy 421 ATACTGCTTTCTGGTAATATGGCCCATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480  
Db 421 GTGCTGGCTTTCTTAGTAATGGCCCATGATTTCTAGTTTCAGAGTCTTGAAGCA--- 476  
Qy 481 ACAGAACACAAAGGACTCTGAGCTCTGGCTTGTGTTACAGAGTGGTACATCTCCACATTACA 540  
Db 477 --TGAAGTAGTGAATGTAACCTGGATTTTTTTTCGGAATGGTATACCTCTGGCATCACA 534  
Qy 541 ATGCTTTTGAATTTCTGTCTTCTGTCTCATCTCTGTGGCTTATTTCAATGTACAGATTTC 600  
Db 535 TCATTTCTGGAATTCGTGATCCCATGTCATCTTAGTCTGCTTATTTCAACATGAATATTTAT 594  
Qy 601 TGGAGCTGTGGAAGCTAGGCTCTCAGTAGTGGCTTACGATGTCCTGATGTTCTCCACT 660  
Db 595 TGGAGCTGTGGAAGCTGATCATCTCAGTAGTGGCTTACGATGTCCTGATGTTCTCCACT 654  
Qy 661 ACCTCTTCCAGTGTCTCAGACACTTACACAGAGCTGGGCTGCTTGCAGGACAGTAAT 720  
Db 655 GTCTCTTCCAACTCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714  
Qy 721 CTTGGAATGAAGAAATCAGCTGCTCATCTCAGTCACTCAGAAAGTCTCTGAAAGAGAGCAGC 780  
Db 715 TCTGCAATGACAGAAATCTCTGATCTCTTCAATTCAGAGACAGAGGAGAAAGATAGT 774  
Qy 781 ATCTCGTGTCTTAAGACTCATAGAACAGAGATATCATCTGCTTCAAAATGGGTTC 840  
Db 775 CTGATGTTTCTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCAAAATGGGTTC 834  
Qy 841 TTTCTGCGATCGAAAGTGCAGCGCTTCGCAAGGAGTACGACAGCTTCTCAGAGGC 900  
Db 835 TTTCTCCAAATCAGATTTCTGTAGCTCTTCAACAAAGGAAACATGTTGAATCTGTAGAGCC 894  
Qy 901 AGAAGCTAGCCAGTCACTGGCCATCTTCTCAGAGCTTTTTCGCAATTTGCTGGGTCCA 960  
Db 895 AGGAGATTAGCCAAAGTCACTGGCAATCTCTTAGGGGTTTGTCTGTGCTGGGTCCA 954  
Qy 961 TACTGTCTGTACAAATGCTCTTCAACTTACCCAGAACGGAAACGCCCAATCGGTG 1020  
Db 955 TATTCTCTGTTCAAATTTGCTTCTTCAATTTATTCCTCAGAACAGGTCTCTAAATCAGTT 1014  
Qy 1021 TGTGACAGCAATGCTTCTGGCTGCAATGTTCAATTCGTTTGAATTCCTTCTGTAC 1080  
Db 1015 TGTATAGAAATGCAATTTGGCTTCAGTGTTCATCTTCTTGTCAATCTCTTTTGTAT 1074  
Qy 1081 CTTTGTGTACAGGCGTTTTCAGAGAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140  
Db 1075 CCATTTGTGTACAGGCGTTTCAAAAGGCTTCTTCAAAATTTTGTATATAAAGCAA 1134  
Qy 1141 CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTGA 1176  
Db 1135 CCTCTACCATCAACACACAGCTGGTCAAGTATCTTCTTAA 1173

RESULT 12

ABK12959  
ID ABK12959 standard; DNA; 1266 BP.

XX AC ABK12959;

XX AC 09-APR-2002 (first entry)

XX DT DNA sequence of human G-protein coupled receptor TGR62 gene.

XX KW Human; G-protein coupled; receptor; GPCR; TGR62; kidney disease; signal transduction modulator; cerebral cavernous malformation; ds; hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure; nephritis; hypertension; liver disease; cirrhosis; blood disorder; spleen-associated disorder; immune disorder; gene; chromosome 18p11.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
CDS 25..1195  
/\*tag= a  
/product= "Human G-protein coupled receptor TGR62"  
XX W0200200719-A2.  
XX 03-JAN-2002.  
XX 25-JUN-2001; 2001WO-US020363.  
XX 23-JUN-2000; 2000US-0213461P.  
XX (TULA-) TULARIK INC.  
XX Lin DC, Zhao J, Chen J, Cutler G;  
XX WPI; 2002-147880/19.  
XX P-PSDB; AAU74906.  
XX New G-protein coupled receptor polypeptides, useful for identifying modulators of signal transduction for treating kidney disease, hyperlipidemia, obesity, dyslexia and cardiac myxoma.  
XX Claim 7; Page 60-61; 78pp; English.  
XX The present invention relates to a new G-protein coupled receptor (GPCR) polypeptide comprising greater than 70% amino acid sequence identity to the amino acid sequence of human GPCRs TGR62, TGR130.1, TGR130.2, human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18 or 90% amino acid sequence identity to human novel edg receptor protein, as defined in the specification. The GPCR covalently linked to a solid phase is useful for identifying a compound that modulates signal transduction. The identified compounds are useful for treating kidney disease, cerebral cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac myxoma. The molecules of the invention are useful for diagnosing disorders or conditions such as kidney-related conditions or diseases such as renal failure, nephritis, nephrotic syndrome, asymptomatic urinary abnormalities, renal tubule defects, hypertension and nephrolithiasis, liver-related disease or condition e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice and spleen-associated disorders or conditions e.g. splenic enlargement, immune disorders, blood disorders and others. Modulation of the polypeptide of the invention is useful to treat or prevent any of the above conditions or diseases. The present nucleic acid sequence is that of the human GPCR TGR62 gene located on chromosome 18p11 and encodes the human GPCR TGR62 protein of the invention. This sequence encodes one of seven novel G protein coupled receptors of the invention (ABK12957- ABK12964)

XX Sequence 1266 BP; 317 A; 268 C; 242 G; 439 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 6; Length 1266;  
Best Local Similarity 75.1%; Pred. No. 2.6e-204;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCCCTTGGCATTTT 60  
Db 25 ATGCCAGATACATAAGCAATCAATATATCAATAGCACTCGGTACTTTAGCATTT 84  
Qy 61 TTAATGTCCTCATTTGCTTTGCTATAATGGTAGGAATGCTGTGTCATCTTAGCCTTT 120  
Db 85 TTTATGTCCTTAGTACTTTTGTCTATAATGCTAGGAATGCTTTGTCATTTAGCTTTT 144  
Qy 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180



145 GTGTGGCAAAACCTTAGACATCGAAGTAGTATATTTTCTTAATCTGGCATCTCT 204  
181 GACTTCCTCGTGGGTTTGAATTCATTCCTCTGTACATCCCTCAGTGTGTTAACTGG 240  
205 GACTTCCTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCAGCGTGTTCGAATGG 264  
241 AATTTTGAAGTGAATCTGATGCTGCTATTTGGCTCAATTAATGACTATCTTTGTGCAACGCA 300  
265 GAATTTGGAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 324  
301 TCTCTCTACAAATATTCCTCATTTAGCTTACATCGATACCATCAGTTCAGATTCCTGCTG 360  
325 TCTGTATATACATGTCCTCATGATGATGATGATGATGATGATGATGATGATGATGATG 384  
361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATGTTGTCAAAATGGTGGCTGTTTGG 420  
385 TCTTATAGAACTCAACATACCTGGGTCTTGAAGATTTGTTACTGATGGTGGCGGTTTGG 444  
421 ATACTGGCTTTCTTGGTAAATGGCCGATGATCTGGCTTCAGATTCCTTGAAGAACAGC 480  
445 GTGTGGCTTTCTTAGTGAATGGGCCAATGATTTCTAGTTCCTGAGATCTTGAAGA--- 500  
481 ACGAACACAAAGGACTGTGAGCTGGCTTCTGTACAGAGTGGTATCATCTCCACCATTACA 540  
501 --TGAAGTAGTGAATGTAACCTGGATTTTTTTCGGAATGTATCTTCCCATCACA 558  
541 ATGCTCTTGGAAATTCCT 600  
559 TCAATCTTGGAAATTCGTATCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618  
601 TGGAGCTGTGAAGCGTAGGCTCTCAGTAGTGGCCCTAGCATCTCTGATTCCTCACT 660  
619 TGGAGCTGTGAAGCGTAGCATCTCAGTAGTGGCCCAAGCCATCTCTGAGTCTGACTGCT 678  
661 ACCTCTTCCAGTCTTCCAGGACACTTAACAAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720  
679 GTCTCTTCCACATCTGTGGACACTTATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 738  
721 COTGAAATGAAGGAATCAGTCTCATCTCGTCTACTCAGAAAGTCTCAGAAAGAGCAGC 780  
739 TCTGATCGACAGAAAGTCTCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 798  
781 ATCTCTGTGCTTGAAGACTCAGATGACAGACAGTATCACTGCTTCAAGTGGGTCTCC 840  
799 CTCTATGTTTCTCAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAGATGGGTCC 858  
841 TTCTGGCGATCGAAAGTCCAGCGCTTCCCAAGGGAGTACGCGAGCTTCTCAGAGGC 900  
859 TTCTCCCAATCAGATCTGTAGCTCTTCCAAAGGGAACATGTTGAACCTGTAGAGCC 918  
901 AGGAAGTAGCAGGTCATCTGGCCATCTCTTGTAGCGCTTTTGGCCATTTGCTGGGCTCA 960  
919 AGGAGATAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTGTTGGGCTCA 978  
961 TACTGTCTCTTCAATCTCTCTTCAACTTACCCAGAACGAAAGCCCAAAATCGGTG 1020  
979 TATCTCTCTTCAATCTCTCTCTTCAATTTATCTCTCAGAACAGGCTCTAAATCAGTT 1038  
1021 TGGTACAGATTCGCTTCTGGGTGCAATGTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080  
1039 TGGTATAGAAATTCATTTTGGCTTCACTGTTTCAATTCCTTGTCAATCTCTTTGTAT 1098  
1081 CTTTGTGTACAGGCGTTTCAGAGGCTTCTGGAAGATCTTGTGTGCAAGCA 1140  
1099 CCAATGTGTCAAGCGCTTTCAAAAGGCTTCTTGAAGATATTTTGTATAAAAGCAA 1158  
1141 CAGCGCTCTCAGAAC---CAGTCAGTATCTTCTTGA 1176  
1159 CTTCTACCAATCAACACAGTCGGTCAGTATCTTCTTAA 1197

ABA02496  
ID ABA02496 standard; DNA; 1300 BP.  
XX  
AC ABA02496;  
DT 26-MAR-2002 (first entry)  
XX  
DE Human G protein-coupled receptor nGPCR-2067-encoding DNA.  
XX  
KW Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor;  
KW signal transduction; mental disorder; central nervous system disease;  
KW metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder;  
KW psychotic disorder; Huntington's disease; schizophrenia; migraine;  
KW depression; anxiety; bipolar disorder; dementia; Alzheimer's disease;  
KW Parkinson's disease; proliferative disorder; cancer; psoriasis;  
KW benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia;  
KW thyroid disorder; cardiovascular disease; hypotension; hypertension;  
KW thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis;  
KW inflammatory conditions; autoimmune disorder; rheumatoid arthritis;  
KW hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic;  
KW antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic;  
KW cardiant; antiatherosclerotic; neuroleptic; antimigraine;  
KW antiparkinsonian; tranquiliser; antidepressant; neuroprotective;  
KW anticonvulsant; antiinflammatory; antirheumatic; antiarthritic;  
KW antipsoriatic; gene therapy; gene; ds.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 41..1213  
FT /\*tag= a  
FT /product= "Human nGPCR-2067"  
XX  
PD WO200185793-A2.  
XX  
XX 15-NOV-2001.  
XX  
XX 08-MAY-2001; 2001WO-US014750.  
XX  
XX 08-MAY-2000; 2000US-0203108P.  
XX  
XX (PHAA ) PHARMACIA & UPOHNN CO.  
XX  
XX Lind P, Sejlitz T, Vogeli G, Wood LS;  
XX  
XX WPI: 2002-062240/08.  
XX  
XX P-PSDB; AAM53050.  
XX  
XX New polynucleotide, useful for identifying modulator compounds which are  
XX used for treating psoriasis, schizophrenia, diabetes, encodes the novel G  
XX protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067).  
XX  
XX Claim 4; Page 62-63; 100pp; English.  
XX  
XX This sequence represents a polynucleotide encoding a novel human G  
XX protein-coupled receptor (GPCR) designated nGPCR-2067. Like all GPCRs,  
XX nGPCR-2067 has 7 putative transmembrane domains and is involved in signal  
XX transduction. The invention also relates to expression vectors and host  
XX cells comprising nucleic acids encoding nGPCR-2067, to recombinant  
XX expression of nGPCR-2067, to antibodies specific for nGPCR-2067, to drug  
XX screening methods that use nGPCR-2067, and to modulators of nGPCR-2067  
XX activity. nGPCR-2067 nucleic acid sequences may be used to isolate nGPCR-  
XX 2067 allelic variants and species homologues and may also be used in  
XX genetic mapping. The invention also discloses the use of nGPCR-2067  
XX nucleic acids in screening for a predisposition to nGPCR-2067-associated  
XX hereditary mental disorders, or for the diagnosis of these disorders.  
XX nGPCR-2067 nucleic acids may additionally be used to generate transgenic  
XX animals, including knockout animals, which may provide an insight into  
XX treating a variety of human disorders, and may also be used in the design  
XX of antisense molecules for suppressing expression of nGPCR-2067 in cells.  
XX nGPCR-2067, and nGPCR-2067 modulators may be used to treat a wide variety  
XX of medical conditions, particularly mental disorders, central nervous  
XX system diseases, and metabolic diseases. Diseases that may be treated



CC include viral infections, particularly HIV-1 or HIV-2 infections; pain;  
CC central nervous system, neurological and psychotic disorders such as  
CC Huntington's disease, schizophrenia, migraine, depression, anxiety,  
CC bipolar disorder, dementia, Alzheimer's disease, and Parkinson's disease;  
CC proliferative disorders such as cancers, benign prostatic hypertrophy and  
CC psoriasis; metabolic disorders such as diabetes, dyslipidaemia, obesity,  
CC and anorexia; thyroid disorders; cardiovascular diseases such as  
CC hypotension, hypertension, thrombosis, myocardial infarction,  
CC cardiomyopathies, and atherosclerosis; inflammatory conditions;  
CC autoimmune disorders (e.g., rheumatoid arthritis); hormonal disorders;  
CC and renal failure  
XX  
SQ Sequence 1300 BP; 324 A; 275 C; 245 G; 456 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 6; Length 1300;  
Best Local Similarity 75.1%; Pred. No. 2.6e-204;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCACACAGTCTCAGTCCCTTGGCAATTT 60  
DB 41 ATGCCAGATACTAATAGACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 100  
QY 61 TTAATGCTTCATTTGCTTGTCTATTAATGGTAGGAAATGCTGTGTCATCTTAGCCCTTT 120  
DB 101 TTTATGTCCTTAGTAGCTTTTGTATTAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 160  
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180  
DB 161 GTGGTGACAGAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCAATCTCT 220  
QY 181 GACTTCTCTGGGTGTGATTCATTCCTCTGTACATCCCTCAGCTGTGTTTAACTGG 240  
DB 221 GACTTCTCTGGGTGTGATTCATTCCTCTGTACATCCCTCAGCTGTGTTTAACTGG 280  
QY 241 AATTTTGGAGTGAATCTGCATGTTTGGCTCAATCTACTGACTATCTTTTGTGCACGCA 300  
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QY 301 TCTGTCTACAATATTGTCCTCAATAGTACGATCGATPACACAGTCAGTTCCTCAATGCTGTG 360  
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QY 421 ATACTGGCTTCTTGTGAATGSCCGCATGATCTGCTTCAGATCTTGGTGAAGAACAGC 480  
DB 461 GTGCTGGCTTCTTGTGAATGGGCCAATGATCTAGTTTTCAGAGTCTTGGAAAGGA--- 516  
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QY 601 TGGAGCTGTGGAAGGTAGGCTCTCAGTAGTGCCCTAGCCATGCTGGAATCTCCACT 660  
DB 635 TGGAGCTGTGGAAGGTGATCATCTCAGTAGTGCCCAAGCCATCCTGCACTGCTGCT 694  
QY 661 ACCTCTTCCAGTCTTTCAGGACATTTACACAGAGTGGGCTGGCTGAGGCAAGTAAT 720  
DB 695 GTCTCTTCCAACTCTGTGACACTATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 754  
QY 721 CTTGGATGAAGAAATCAGTGCATCTCGTCACTCAGAAAGTCTCTCGAAAGAAAGACAGC 780  
DB 755 TCTGCATCAGACAAAGTTCCTGCTATCTTTTCAATTCAGAGACAGAGGAGAAAGTACT 814  
QY 781 ATCTGCTGCTCTTATAGGACTACATGAACAGCAGTATCACTGCTTCAAGTGGGTCC 840  
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QY 841 TTCTGGCATCGAAGTGTGAGCCTTCGCCAAGAGGAGTACGAGAGCTTCTCAGAGGC 900  
DB 875 TTCTCCCAATCAGATTCTGTAGCTCTTTCACCAAGGGAACATGTTGAATCTCTTAGAGCC 934  
QY 901 AGAAGCTAGCCAGTCACTGGCCATCCTTCTGAGCGCTTTTGCATTTGCTGGCTCCA 960  
DB 935 AGGAGATTAGCCAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 994  
QY 961 TACTGTCTGTCAATTTGCTTCACTTACCTTACCCAGAACGGAACGCCCAATTCGGTG 1020  
DB 995 TATTCTCTGTTCACAATTTGCTTCACTTATTTCTCAGCAACAGCTCCTAATCAGTT 1054  
QY 1021 TGGTACAGCATTTGCTTCTGGCTGCAATGTTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080  
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QY 1081 CCTTTGTCACAGGCGTTTCCAGAGGCTTCTGGAAGTACTTTGTGTGACAAAGCAA 1140  
DB 1115 CCATTGTGTCAAGCGCTTTCAAAGGCTTCTTGAATAATTTTGTATAAAAGCAA 1174  
QY 1141 CCAGCGCTGTCAAGAAC---CAGTCACTATCTTCTTGA 1176  
DB 1175 CCTCTACCATCAACACACAGCTCGTCACTATCTTCTTAA 1213

## RESULT 14

AAH47911

ID AAH47911 standard; cDNA; 1312 BP.

XX AAH47911;

AC AC

DT 25-SEP-2001 (first entry)

XX Human G protein-coupled receptor protein BG26 encoding cDNA.

DE Human; G protein-coupled receptor protein BG26; histamine H3; histamine;  
KW altering intracellular cAMP concentration;  
KW regulating signal transduction; ss.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 64..1236

FT /\*tag= a

FT /product= "G protein-coupled receptor BG26"

XX WO200146414-A1.

XX 28-JUN-2001.

XX 20-DEC-2000; 2000WO-JP009038.

XX 20-DEC-1999; 99JP-00361687.

XX (BANY ) BANYU PHARM CO LTD.

XX Itadani H, Nakamura T, Tanaka K, Ohta M;

XX WPI; 2001-441675/47.

XX P-PSDB; AAG64477.

XX G protein-coupled receptor protein BG26, with activity of binding to  
PT histamine and capable of changing intracellular cAMP concentration in  
PT response to its stimulus, applicable as tool in screening ligands or drug  
PT candidates.

XX Claim 1; Page 37-41; 50pp; Japanese.

XX The present sequence is that of the human G protein-coupled receptor  
CC protein BG26 encoding cDNA, which shows significant homology with  
CC histamine H3, with activity of binding to histamine and capable of  
CC changing intracellular cAMP concentration in response to its stimulus.

CC	The protein is applicable as a tool in screening ligands or drug candidates for regulating signal transduction from such protein and CC treating diseases associated with its abnormality
xx	Sequence 1312 Bp; 326 A; 276 C; 251 G; 459 T; 0 U; 0 Other;
sq	Query Match 58.4%; Score 686.6; DB 4; Length 1312; Best Local Similarity 75.1%; Pred. No. 2.6e-204; Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
QY	1 ATGTCGGAGTCTAAACAGTACTGGCATCTTGCCACACAGCTGCTCAGGTCCCGCTTGGCAATT 60
Db	64 ATGCCAGATACATAAGACAAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCAATT 123
QY	61 TTAATGTCTTCATTTGGCTTTGCTATAATAGTAGCAATGCTGTGTCATCTTAGCCCTTT 120
Db	124 TTTATGTCTTAGTAGCTTTTGCTATAATAGCTAGAAATGCTTTGGTCATTTAGCTTTT 183
QY	121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTCT 180
Db	184 GTGGTGACAAACCTTAGACATCGAAGTAGTATTTTTTCTTAACCTGGCCATCTCT 243
QY	181 GACTTCCTCGGGTTGATTTCCATTCCTCTGTATACCTCCACAGTGTGTTTAACCTGG 240
Db	244 GACTTCCTTGTGGGTGTGATCTCCATTCCTTTGTATACATCCCTCACAGCTGTGGCAATGG 303
QY	241 AATTTTGAAGTGAATCTGCATGTTTGGCTCAATTAAGTACTATCTTTTGTGCAACCGCA 300
Db	304 GATTTTGAAGAGAAATCTGTATTTTGGCTCACTAGTACTATCTGTATGTATACAGCA 363
QY	301 TCTGTCTACAATATTGTCTCTCATTTAGCTACGATACGATACCAAGTCAGTTTCAAACTGTG 360
Db	364 TCTGTATATAACAATTTGCTCTCATCAGCTATGATGATACCTGTCACTTCAAACTGTG 423
QY	361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAACTGGTGGCTTTGG 420
Db	424 TCTTATAGAATCTCAACACTACTGGGGCTCTGAAGATTGTACTTCTGATGGTGGCCGTGG 483
QY	421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTTCTGGGCTTCAGATTCTTTGGAAGAACAGC 480
Db	484 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTTGAAGGA --- 539
QY	481 ACGAACACAAGAGACTGTGAGCTGGCTTTGTTACAGAGTGGTATCATCTCACCAATTACA 540
Db	540 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTATCATCTTGCCATACA 597
QY	541 ATGCTCTTGGAAATTCCTGCTTCTGCTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600
Db	598 TCATTTCTTGGAAATTCGTATCCAGTATCATTTAGTCGCTTATTTCAACATGAATATTAT 657
QY	601 TGGAGCCTGTGGAACGCTAGGCTCTCATAGTAGTGCCCTAGCCATCTGGATTTCCACT 660
Db	658 TGGAGCCTGTGGAACGCTGATCATCTCAGTAGTGCCAAAGCCATCTTGGACTGCTGT 717
QY	661 ACCTCTTCAGTGCTTCAGGACACTTACACAGCTGGGGTGGCTGCAAGGCAAGTAAT 720
Db	718 GTCTCTTCCAGCATCTGTGAGCACTCATTTCAAGGTAGACTATTTTCAAGGAGATCTCTTT 777
QY	721 CTTGGATTGAAGGAATCAGCTGCATCTCGCTCACTCAGAAAGTCTTCGAAAGAGAGCAAC 780
Db	778 TCTGCATCGACAGAAGTTCTTGATCTCTTCAATTCAGAGAGACAGAGGAGAAAGTAGCT 837
QY	781 ATCTTGTTGCTTTAAGGACTCACATGAACAGCAGTATCATCTGCCCTTCAAGTGGGTTC 840
Db	838 CTCATGTTTTCCTCAGAAACCAAGATGAATAGCAATACAAATTTGCTTCCAAAATGGGTTC 897
QY	841 TTTCTGCGATCGAAAGTCCAGCGCTTCCGCAAAAGGAGTACGACAGCTTCTCAGAGGC 900
Db	898 TTCTTCCAAATCAGATTCGTAGTCTTTTACCAAGAGGAACATGTTGAATGCTTTAGGCC 957
QY	901 AGGAAGCTAGCAGGTCACCTGGCCATCTCTTCTAGCGCTTTTGGCCATTTGCTGGGCTCCA 960
Db	958 AGGAGATTTAGCAAGTCACTGGCCATTTCTTTAGGGGTTTTTGTCTGTTTGTGGGCTCCA 101

presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases. Growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

Sequence 3689 BP; 975 A; 739 C; 746 G; 1229 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 7; Length 3689;  
Best Local Similarity 75.1%; Pred. No. 4.6e-204;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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QY 1 ATGTCGAGCTACACGACTGCGCATCTTGCACACGCTGCTCAGGTCCTGGCAATTT 60
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 TTAATGCTTTCATTTGCTTTGTATATATGCTAGGCAATGCTGGTCATCTTAGCCCTT 120
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 401 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTCACTCAAAATGCTGTG 460
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QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGTGTGCTCAAAATGGTGGCTGTTTG 420
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QY 521 GTGCTGGCCCTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGAAGGA---- 576
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 721 CTTGGATTGAAGGAATCAGCTGCTCATCTCGTCACTCAGAAAGTCTCTCGAAGAAAGACAGC 780
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Job time : 568 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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5932.930 Million cell updates/sec

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	143.2	12.2	1338	US-09-165-543-6	Sequence 6, Appli
4	143.2	12.2	3244	US-09-165-543-4	Sequence 4, Appli
5	140.4	11.9	1335	US-08-985-090-3	Sequence 3, Appli
6	140.4	11.9	1335	US-09-165-543-3	Sequence 3, Appli
7	140.4	11.9	1335	US-09-167-354-6	Sequence 6, Appli
8	140.4	11.9	1335	US-09-642-855-6	Sequence 6, Appli
9	140.4	11.9	1335	US-09-642-514-6	Sequence 6, Appli
10	140.4	11.9	2689	US-08-985-090-1	Sequence 1, Appli
11	140.4	11.9	2689	US-09-165-543-1	Sequence 1, Appli
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15	94	8.0	1086	US-08-985-090-6	Sequence 6, Appli
16	94	8.0	1086	US-09-165-543-33	Sequence 33, Appli
17	94	8.0	2218	US-08-985-090-4	Sequence 4, Appli
18	94	8.0	2218	US-09-165-543-31	Sequence 31, Appli
19	93.8	8.0	1056	US-09-524-162-1	Sequence 1, Appli
20	67.6	5.7	2210	US-09-016-434-1177	Sequence 1177, Ap
21	64.4	5.5	2261	US-09-016-434-1176	Sequence 1176, Ap
22	61.2	5.2	1233	US-09-721-870-176	Sequence 176, App
23	59	5.0	1913	US-09-016-434-1314	Sequence 1314, Ap
24	57.6	4.9	1579	US-09-016-434-1243	Sequence 1243, Ap
25	56.8	4.8	2595	US-09-016-434-1178	Sequence 1178, Ap
26	56	4.8	1386	US-09-016-434-1339	Sequence 1339, Ap
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28	56	4.8	1581	3	US-08-767-993-8	Sequence 8, Appli
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45	48.4	4.1	1239	1	US-08-349-696-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1

US-09-414-010-1  
; Sequence 1, Application US/09414010  
; Patent No. 6204017  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monsma, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414,010  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-414-010-1

Query Match	58.4%	Score	686.6	DB	3	Length	1173
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QY 961 TACTGTCTCTTCACAATTTCTCTTTTCAACTTACCCAGAAAGGAGCGCCCAATCGGTG 1020  
Db 955 TATTCTCTGTTCACAATTTCTCTTTTCAATTTATCTCTCAGAACAGGTCTTAAACAGTT 1014  
QY 1021 TGGTACAGATTCCTTCTGCTGCAATGTTTCAATTCGTTTGTAAATCCCTTTCTGTAC 1080  
Db 1015 TGGTATAGAAATTCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTGTAT 1074  
QY 1081 CTTTGTGTGCACAGGCTTCAGAAAGGCTTTCTGGAAGATTTTGTGTGACAAAGCAA 1140  
Db 1075 CAAATGTGTCAAGCGCTTTCAAAAGGCTTTCTTGAAATATTTTGTATAAAAAAGCAA 1134  
QY 1141 CCAGCGCTCTCACAGAAC--CAGTCAGTATCTTCTTGA 1176  
Db 1135 CTTCTACCATCAACACAGTCGGTCAGTATCTTCTTAA 1173

## RESULT 3

US-09-165-543-6  
; Sequence 6, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1338 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1335

US-09-165-543-6

Query Match 12.2%; Score 143.2; DB 3; Length 1338;  
Best Local Similarity 54.2%; Pred. No. 3e-35;  
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

QY 3 CTCGGAGTCTAAACAGTACTGGCATCTTGGCACAGCTGCTCAGGTCCCTTGSCATTTTT 62  
Db 60 GCGCGCTGCAGCGGGGCGCGCGCTTCTCGGCTGCTCGACCGCTGTCTCTGGCTGGCT 119  
QY 63 AATGTCTTCAATTTGCCCTTTGCTTATATGTTAGCAATGCTGTGGTCACTCTTACCCCTTTGT 122  
Db 120 CATGGGCTGCTCATCGTGGCCACAGTACTGGGCAACGGCTGGTCACTGCTGCCCTTCGT 179  
QY 123 GTTGACAGAAACCTTAGACATCGAAGTAATTAATTTTTTTTAAATTTGGCTATTTCTGA 182  
Db 180 GCGGATTCGAGCTCGCGCACCAAGAACTCTTTCTGCTCAACTCGCCATCTCCGA 239  
QY 183 CTTCTCTCTGGGTTGATTTCCATTTCTCTGTACATCCCTCAGGTGTTTAAAC---TG 239  
Db 240 CTTCTCTGGGTTGCTTCTGATCCCATTTGACGTACCTATGCTGTGCTGACCGCGCTTG 299  
QY 240 GAATTTTGAAGTGAATCTGATGTTTTGGCTCAATCTACTGACTATCTTTTGTGACCGC 299  
Db 300 GACCTTCGCGCGGCGCTCTGCAAGCTGTGGTGGTGGTAGACTTACCTACTGTGGCTC 359  
QY 300 ATCTGTCTACAATATTGTCCTCATTTAGCTACGATCGATACCACTCAGTTTCAAACTGCT 359  
Db 360 CTCGGCTTCAACATCGTACTCATCAGCTATGACCGATTCTCTGTCAGTCACTCGAGCT 419  
QY 360 GTCTTATAGGCTCAACACATCGGCTCATGAAGATTGTTGCTCAAAATGGTGGCTGTTG 419  
Db 420 CTCCTACAGGGCGCCAGCAGCGGCGCTTCGGAAGATGGCACTGGCTG 479  
QY 420 GATACTGCTTTCTTGGTAAATGGCGCGATGATCTGCTTCAGAA-----TTCTTGGAA 473  
Db 480 GGTGCTGCGCTTCTGCTGTATGGGCTTGCATCTGAGTTGGAGTACTGCTGGTGG 539  
QY 474 GAACAGCAGCAACAAAGGACTGTGAGCCTGTGAGCCTGCTTTGTTACAGAGTGGTACATCCTAC 533  
Db 540 CAGTTCCATCCCGAGGCGCACTGCTATGCTGAGTTCTTCTACAAGTGGTACTTCTCAT 599  
QY 534 CATTAACAATGCTTTGGAATCTCTCTCTCTGCTCACTCTGCTGGCTATTTCAATGTACA 593  
Db 600 CAGGCGCTCCACCTCGAGTTCTTCAAGCGCTTCTCAGCGTTACCTTCTTCAAGCTCAG 659  
QY 594 GATTTACTGGAGCCTGTGGAAGCGTA 619  
Db 660 CATCTACTGACATCCAGAGCGCA 685  
RESULT 4  
US-09-165-543-4  
; Sequence 4, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth A. Hanley  
REGISTRATION NUMBER: 33,505  
REFERENCE/DOCKET NUMBER: MNI-032CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 778..2112  
US-09-165-543-4

Query Match 12.2%; Score 143.2; DB 3; Length 3244;  
Best Local Similarity 54.2%; Pred. No. 5.1e-35;  
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;  
QY 3 GTGGAGTCTAACAGTACTGGCATCTTGGCCACCAAGTCTCAGTCCCTTGGCATTTT 62  
DB 837 GCGGCTGACGGCGGGCGGGCTTCTGGCTGCTGGACCGCTGCTCTGGCTGGCT 896  
QY 63 AATGCTTTCATTTGCCCTTGTATTAATGTAAGGAATGCTGTGGTCACTTAGCCTTGT 122  
DB 897 CATGGCCTGCTCATCTGCGCCACAGTACTGGGCAACGCGCTGCTGCTGCGCTTGT 956  
QY 123 GTGGACAGAACTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCTGA 182  
DB 957 GCGGATTCGAGCTTCGACCCAGAACACTTCTTCTGCTCACTCGCATCTCGA 1016  
QY 183 CTTCCTCGTGGTGTGATTTCCATTCCTGTATACCTCCCTCACTGTTGTTTAAAC---TG 239  
DB 1017 CTTCCTCGTGGTGGCTTCTGCATCCCATTTGATGCTACCTTATGCTGCTGACCGCGCTG 1076  
QY 240 GAATTTTGGAGTGGATCTGCATGTTTGGCTCACTACTGACTATCTTTTGTGACCGC 299  
DB 1077 GACCTTCGCGGGGGCTCTGCAAGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1136  
QY 300 ATCTGTCTACAATTTGCTCTATTAGTACGATCGATACCAAGTCTGAGTTCCTCAATGCTGT 359  
DB 1137 CTGGTCTTCAACATCGTACTCATCAGTATGACGGAATCTCTGTCACTCATCGAGCTGT 1196  
QY 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGTGGTGG 419  
DB 1197 CTCCTACAGGCGCCAGCAGGGGGACACGAGACGGCGCGTTCGGAAGATGGCACTGGTGTG 1256  
QY 420 GATCTGGCTTCTTGTGAATGCGCGGATGATTTGCTTCAG-----TTCTTGGAA 473  
DB 1257 GGTCTGGCTTCTTGTGAATGCGCGGATGATTTGCTTCAG-----TTCTTGGAA 473  
QY 474 GAACAGACGAAACAAAGGACTGTGAGCTGGCTTGTACAGAGTGGTATCTCTCAC 533  
DB 1317 CAGTTCATCCCGAGGGCACTGCTATGCTGAGTCTTCTTCACTGGTACTTCTCAT 1376  
QY 534 CATTAACATGCTTGTGAATTCCTGCTTCTGCTCATCTCTGCTGCTTATTTCAATGTACA 593  
DB 1377 CACGGCTCCACCTCGAGTTCTTACGCCCTTCTCAGCGCTTCTCAGCGCTTCTTCTTCAACCTCAG 1436  
QY 594 GATTACTGGAGCTGTGGAGCGTA 619  
DB 1437 CATCTACTGAACATCCAGAGCGCA 1462

RESULT 5  
US-08-985-090-3  
; Sequence 3, Application US/08985090  
; Patent No. 5885893  
; GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl  
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,090  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jean M. Silveri  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MNI-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1335 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1335  
US-08-985-090-3

Query Match 11.9%; Score 140.4; DB 2; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 2.3e-34;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;  
QY 3 GTCCGAGTCTAACAGTACTGGCATCTTGGCCACCAAGTCTCAGTCCCTTGGCATTTT 62  
DB 60 GCGCGCGGGCGGGCGGGCTTCTGGCAGCTGGACCGGCTGGCGCGCT 119  
QY 63 AATGCTTTCATTTGCCCTTGTATTAATGTAAGGAATGCTGTGGTCACTTAGCCTTGT 122  
DB 120 CATGGCCTGCTCATCTGCGCCACAGTCTGGGCAACGCGCTGCTGCTGCTGCT 179  
QY 123 GTTCGACAGAACTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCTGA 182  
DB 180 GCGGATTCGAGCTTCGACCCAGAACACTTCTTCTGCTCACTCGCATCTCGA 239  
QY 183 CTTCCTCGTGGTGTGATTTCCATTCCTGTATACCTCCCTCACGTTG---TTTAACTG 239  
DB 240 CTTCCTCGTGGCGCTTCTGCATCCCATGTATGACCTACGCTGACGAGCGCGCTG 299  
QY 240 GAATTTTGGAGTGGAAATCTGCATGTTTGGCTCACTACTGACTATCTTTTGTGACCGC 299  
DB 300 GACCTTCGCGCGGGCTCTGCAAGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 359  
QY 300 ATCTGTCTACAATTTGCTCTATTAGTACGATCGATACCAAGTCTGAGTTCCTCAATGCTGT 359  
DB 360 CTTCGCTTCAACATCGTGTCTCATGCTACGACGCTTCTGCTGGTCACTCGGAGCGGT 419  
QY 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAATGCTGGTGGTGGT 419  
DB 420 CTCATACCGGCGCCAGCAGGGGTGACACGCGCGGGCAGTGGCGAAGATGCTGCTGGTGG 479  
QY 420 GATCTGGCTTCTTGTGGTAAATGGCCCCGATGATCTGCTTCAGAT-----TCCTTGGAA 473



Db 480 GGTGCTGGCTTCTGCTGTAAGGACGACGATCCTGAGCTGGAGTACCTGTCGGGGG 539  
QY 474 GAACAGACAAACAAAGAGACTGTGAGCTGGCTTTGTACAGAGTGGTACATCTCTAC 533  
Db 540 CAGTCCATCCCGAGGAGCCACTGCTATGCGAGTTCTTCTACAACTGGTACTTCTCT 599  
QY 534 CATTACAAATGCTCTTGAAATTCCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 593  
Db 600 CAGGCTTCCACCTTGAGTCTTACGCGCTTCTCAGGCTACCTTCTTTAACTCAG 659  
QY 594 GATTACTGAGCTGTGGAAGCTAGGCTCTCAG 629  
Db 660 CATCTACTGAACATCCAGAGGCGCACCCGCTCCG 695

## RESULT 6

US-09-165-543-3  
; Sequence 3, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1335 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1335  
US-09-165-543-3

Query Match 11.9%; Score 140.4; DB 3; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 2.3e-34;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;  
QY 3 GTGAGTCTAACAGTACTGTCATCTTGCCACAGCTGCTGAGTCCCTTGGCATTTT 62  
Db 60 GCGCGCGGCGGCGCGGCTTCTCGGAGCTGACCGCGGTGCTGCGCGCT 119  
QY 63 AATGCTTTCATTTGCTTTGCTTATATGTTAGGCAATGCTGTGGTCACTTAGCCCTTGT 122  
Db 120 CATGGCGTGTCTCATGTTGGCCACGCTGTGCGCAACGCGTGGTCTGCTGCTTCTGT 179

QY 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAAATTTGGCTATTTCGA 182  
Db 180 GGGCGACTCGAGCTCCGACCCAGAACTTCTTCTGCTCAACTCGCACTCGCA 239  
QY 183 CTTCTCTGCTGGGTTTGAATTTCCATTCCTCTGTATACATCCCTCAGTGTG---TTTAACTG 239  
Db 240 CTTCTCTGCTGGGCGCTTCTGCAATCCACATGTATGTATCCCTAGCTGCTGACAGCGCGCTG 299  
QY 240 GAATTTTGAAGTGAATCTGCAATGTTTGGCTCAITACTGACTATCTTTTGTGCACCGC 299  
Db 300 GACCTTCGCGCGGCGCTCTGCAAGCTGTGGTGTAGTACTACTCTGCTGTGCACCTC 359  
QY 300 ATCTGTCTACAATATGTCTCTCATTTAGCTAGATCGATACAGTCACTTTCAAATGCTGT 359  
Db 360 CTCTGCTTCAACATCTGCTCATCAGTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 419  
QY 360 GTCTTATAGGCTCAACACACTGSCATCATGAAGATTTGTTGCTCAATGCTGCTGCTGCTGCTGCT 419  
Db 420 CTATACCGGCGCCAGCGGCTGACCGCGCGGCGAGTCCGGAAGATGCTGTGTGTGTG 479  
QY 420 GATACTGGCTTCTTGGTAAATGCGCGATGATTTCTGGCTTCAGAT-----TCTTGGAA 473  
Db 480 GGTGCTGGCTTCTCTGCTGTAAGGACGACCATCTGAGCTGGGAGTACCTGTCCGGGG 539  
QY 474 GAACAGACAAACAAAGAGCTGTGAGCTGGCTTTGTACAGAGTGGTACATCTCTAC 533  
Db 540 CAGTCCATCCCGAGGCGCACTGTATGCGAGTTCTTCTACAACTGGTACTTCTCTCAT 599  
QY 534 CATTACAATGCTCTTGGAAATTCCTGCTTCTGCTCATCTCTGCTGCTTATTTCAATGTACA 593  
Db 600 CAGGCTTTCACCTCGAGTTCTTTAGGCCCTTCTCAGGCTCACCTTCTTAACTCAG 659  
QY 594 GATTACTGAGCTGTGGAAGCTAGGCTCTCAG 629  
Db 660 CATCTACTGAACATCCAGAGGCGCACCCGCTCCG 695

RESULT 7  
US-09-167-354-6  
; Sequence 6, Application US/09167354A  
; Patent No. 6136559  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; TITLE OF INVENTION: SUBTYPE  
; FILE REFERENCE: JMW  
; CURRENT APPLICATION NUMBER: US/09/167,354A  
; CURRENT FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CDNA  
US-09-167-354-6

Query Match 11.9%; Score 140.4; DB 3; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 2.3e-34;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;  
QY 3 GTGAGTCTAACAGTACTGTCATCTTGCCACAGCTGCTGAGTCCCTTGGCATTTT 62  
Db 60 GCGCGCGGCGGCGGCGGCTTCTCGGAGCTGACCGCGGTGCTGCGCGCT 119  
QY 63 AATGCTTTCATTTGCTTTGCTTATATGTTAGGCAATGCTGTGGTCACTTAGCCCTTGT 122  
Db 120 CATGGCGTGTCTCATGTTGGCCACGCTGTGCGCAACGCGTGGTCTGCTGCTTCTGT 179

123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGA 182  
180 GGCGGAGCTCGAGGCTCGCGACCCAGAGAACTTCTCTGCTCAACCTCGGCATCTCCGA 239  
183 CTTCTCTGGTGGTTTGAATTTCCATTTCTCTGTATACATCCCTCACGCTGTG---TTTAACTG 239  
240 CTTCTCTGGTGGGCTCTGCACTCCACCTGTATGTATACCTACGCTGTGACAGCCGCTG 299  
240 GAATTTTGGAAAGTGAATCTGCACTGTGTTGGCTCAATTAAGTACTATCTTTTGTGCACGC 299  
300 GACCTTCGGCGGGGCTCTGCAAGCTGTGCTGTAGTGGACTACCTGTGTGCACTC 359  
300 ATCTGTCTCAAAATTTCTCTCATCTAGTACGATCGATACCAAGTCAGTTTCAAAATGCTGT 359  
360 CTCTGCTTCAACATCTGCTCATCAGTACGACCGCTTCTCTGCGGTCAACCGAGCGGT 419  
360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGTTGGCTGTGTTG 419  
420 CTCTACCGGGCCAGAGGCTGACACGGCGGGCAGTGGGAAGATGCTGTGTTG 479  
420 GATACGCTTCTTGTGAATGCGCCGATGATTTCTGGCTTCAGAT-----TCTTGGAA 473  
480 GGTCTGGCTTCTCTGTGTAGTGGACCAAGCATCTGAGCTGGAGTACCTGTCCGGGG 539  
474 GAAACAGCAGAAACAAAGGACTGTGAGCTGTGCTTGTACAGAGTGGTACATCCTCAC 533  
540 CAGCTCCATCCCGAGGGCCACTGTATGCGAGTCTTCTACAACTGGTACTTCTCAT 599  
534 CATTACAAATGCTCTTGGAAATCTGCTTCTCTCATCTCTGCTGTGGCTTATTTCAATGTACA 593  
600 CACGGCTTCCACCTGGAGTTCTTACGCTTCTCTCAGCGTCACTTCTTTAACTCAG 659  
594 GATTACTGGAGCTGTGGAAGCGTAGGGCTCTCAG 629  
660 CATCTACCTGAACATCCAGAGCGCACCGGCTCG 695

## RESULT 8

US-09-642-855-6  
; Sequence 6, Application US/09642855  
; Patent No. 6413743  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: SUBTYPE  
; CURRENT APPLICATION NUMBER: US/09/642,855  
; CURRENT FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 09/167,354  
; PRIOR FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CDNA  
US-09-642-855-6

Query Match 11.9%; Score 140.4; DB 4; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 2.3e-34;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;  
3 GTGCGAGTCTAACAGTACTGGCATCTTGCACAGCTGTCTCAGTCCCTTGGCATTTT 62  
60 GGCGGGGGGGGGGGGGGGGGCTTCTCGGAGCGCTGACCGCGGTGCTGGCGCGCT 119  
63 AATGCTCTATTGCTTGTCTATAATGGTAGGCAATGCTGGTCACTTAGGCTTTGT 122

120 CATGGCGCTGCTCATCTGGCCACGGTGTGGGCAACGCGCTGTCACTGCTCGCTTCGT 179  
123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGA 182  
180 GGCGGAGCTCGAGGCTCGCGACCCAGAGAACTTCTCTGCTCAACCTCGGCATCTCCGA 239  
183 CTTCTCTGGTGGTGGTTTGAATTTCCATTTCTCTGTATACATCCCTCACGCTGTG---TTTAACTG 239  
240 CTTCTCTGGTGGGCTCTGCACTCCACCTGTATGTATACCTACGCTGTGACAGCCGCTG 299  
240 GAATTTTGGAAAGTGAATCTGCACTGTGTTGGCTCAATTAAGTACTATCTTTTGTGCACGC 299  
300 GACCTTCGGCGGGGCTCTGCAAGCTGTGCTGTAGTGGACTACCTGTGTGCACTC 359  
300 ATCTGTCTCAAAATTTCTCTCATCTAGTACGATCGATACCAAGTCAGTTTCAAAATGCTGT 359  
360 CTCTGCTTCAACATCTGCTCATCAGTACGACCGCTTCTCTGCGGTCAACCGAGCGGT 419  
360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGTTGGCTGTGTTG 419  
420 CTCTACCGGGCCAGAGGCTGACACGGCGGGCAGTGGGAAGATGCTGTGTTG 479  
420 GATACGCTTCTTGTGAATGCGCCGATGATTTCTGGCTTCAGAT-----TCTTGGAA 473  
480 GGTCTGGCTTCTCTGTGTAGTGGACCAAGCATCTGAGCTGGAGTACCTGTCCGGGG 539  
474 GAAACAGCAGAAACAAAGGACTGTGAGCTGTGCTTGTACAGAGTGGTACATCCTCAC 533  
540 CAGCTCCATCCCGAGGGCCACTGTATGCGAGTCTTCTACAACTGGTACTTCTCAT 599  
534 CATTACAAATGCTCTTGGAAATCTGCTTCTCTCATCTCTGCTGTGGCTTATTTCAATGTACA 593  
600 CACGGCTTCCACCTGGAGTTCTTACGCTTCTCTCAGCGTCACTTCTTTAACTCAG 659  
594 GATTACTGGAGCTGTGGAAGCGTAGGGCTCTCAG 629  
660 CATCTACCTGAACATCCAGAGCGCACCGGCTCG 695

## RESULT 9

US-09-642-514-6  
; Sequence 6, Application US/09642514  
; Patent No. 6437100  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: SUBTYPE  
; CURRENT APPLICATION NUMBER: US/09/642,514  
; CURRENT FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 09/167,354  
; PRIOR FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CDNA  
US-09-642-514-6

Query Match 11.9%; Score 140.4; DB 4; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 2.3e-34;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;  
3 GTGCGAGTCTAACAGTACTGGCATCTTGCACAGCTGTCTCAGTCCCTTGGCATTTT 62  
60 GGCGGGGGGGGGGGGGGGGGCTTCTCGGAGCGCTGACCGCGGTGCTGGCGCGCT 119

63 AATGCTTCAATTTGCTTTGCTATAATGTTAGCAATGCTGTGCTCATCTTTAGCCTTTGT 122  
120 CATGGCGTGTCTATCGTGGCCACGGTGTGGCAACGGCTGTGCTCATGCTGCTTGT 179  
123 GGTGGACAGAACCTTAGACATCAAGTAATATTTTCTTAATTTGGCTATTCTGA 182  
180 GGCGACTCGAGCTCCGCCACCCAGAACAACTTCTGCTCAACCTCGCATCTCGA 239  
183 CTTCCTCGTGGGTTTGATTTCCATCTCTGTATACCTCCTCACTGTG---TTTAATG 239  
240 CTTCCTCGTGGCGCTTCTGATCCACATGATGTATGATGATGCTGACAGCCGCTG 299  
240 GAATTTGGAGTGAATCTGCAATGTTTGGCTCAATTAATGCTGATATCTTTTGTGCAACCG 299  
300 GACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGAATGCTGCTGTGCACTC 359  
300 ATCTGCTCAATATTTGCTCATTAATGCTAGGATCGATACAGTCAATTTCAATGCTGT 359  
360 CTCTGCTTCAACATGCTGTCTATCACTAGTACGACCGCTTCTGTGCTGCTGCTGCT 419  
360 GTCTTATAGGGCTCAACACACTGCAATCAATGAAGATTGTTGCTCAATGCTGCTGTTG 419  
420 CTCAATCGGGCCAGAGGCTGACACGGCGGGGAGTGGGAAGATGCTGTGCTGTTG 479  
420 GATACCTGGCTTCTTGTGTAATGCGCGATGATTTGCTGGCTTCAGAT-----TCTTGGAA 473  
480 GGTGCTGGCTTCTGCTGTACGACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 539  
474 GAACAGACAGAACACAAAGAGCTGTGAGCTGGCTTGTGTTGTTGTTGTTGTTGTTGTTG 533  
540 CAGCTCCATCCCGAGGGGCGACGCTATGCGGAGTCTTCTTCAAACTGCTGCTCAT 599  
534 CAATTAATGCTCTTGGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593  
600 CAGGCTTCCACCTGGAGTCTTACGCTTCTTACGCTTCTTACGCTTCTTACGCTTCTT 659  
594 GATTACTGAGCTGTGGAAGCTGAGGCTGCTCAG 629  
660 CATCTACCTGAACATCCAGAGGCGGACCGGCTCCG 695

## RESULT 10

US-08-985-090-1  
; Sequence 1, Application US/08985090  
; Patent No. 5885893  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl  
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,090  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jean M. Silveri  
; REGISTRATION NUMBER: 39,030  
; REFERENCE/DOCKET NUMBER: MNI-032  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2689 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 291..1625  
; US-08-985-090-1

## Query Match 11.9%; Score 140.4; DB 2; Length 2689;

Best Local Similarity 53.6%; Pred. No. 3.5e-34;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

QY 3 GTCGGAGTCTAAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCATTTT 62  
Db 350 GCGCGCGCGCGCGCGCGCGCTTCTCGGAGCCTGGACCGCGGTGCTGCGCGCGCT 409  
QY 63 AATGCTTTCATTTGCTTTGCTATAATGTAGGCAATGCTGTGCTCATCTTAGCCTTTGT 122  
Db 410 CATGGCGCTGCTCATCTGTCGCCACGGTGTGGCAACGGCTGTGCTCATGCTGCTGCT 469  
QY 123 GGTGGACAGAACCTTAGACATCAAGTAATATTTTCTTAATTTGGCTATTCTGA 182  
Db 470 GCGGACTCGAGCTCCGCCACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCGGA 529  
QY 183 CTTCCTCGTGGGTTTGATTTCCATTTCTGTCATATCCCTCAGCTGTTG---TTTAATG 239  
Db 530 CTTCCTCGTGGCGCTTCTGTCATCCACTGATGACCTTACCTGCTGCTGCTGCTGCT 589  
QY 240 GAATTTTGGAGTGAATCTGCTGTTTGGCTTCTTACTGCTTCTTGTGCTGCTGCTGCT 299  
Db 590 GACCTTCGCGCGGCGCTCTGCAAGCTGTGGCTGTAGTGAATGCTGCTGCTGCTGCT 649  
QY 300 ATCTGCTCAATATTTGCTCATTAATGCTAGTACGATACGATACGATGCTGCTGCTGCT 359  
Db 650 CTCTGCTTCAACATGCTGCTCATCAGTACGACCGGCTTCTGCTGCTGCTGCTGCTGCT 709  
QY 360 GTCTTATAGGGCTCAACACACTGSCATCATGAAGATTGTTGCTCAATGCTGCTGCTGCT 419  
Db 710 CTCAACCGGCGCGGCTGACACGGCGGGGAGTGGGAAGATGCTGCTGCTGCTGCT 769  
QY 420 GATCTGCTTCTTGGTAAATGGCCGATGATTTCTGGCTTCTGAT-----TCTTGGAA 473  
Db 770 GGTGCTGGCTTCTGCTGTACGGACCGCATCTGAGCTGGAGTACTGCTCCGGGG 829  
QY 474 GAACAGCAGAACACAAAGGACTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533  
Db 830 CAGCTCCATCCCGGAGGCGCACTGCTATCCGAGTTCTTCTACAACTGCTGCTGCTCAT 889  
QY 534 CATTAATGCTTCTTGGAAATCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593  
Db 890 GAGGCTTCCACCTGGAGTTCTTACGCCCTTCTTACGCTGCTGCTGCTGCTGCTGCT 949  
QY 594 GATTACTGAGCTGTGGAAGCTGAGGCTGCTCAG 629  
Db 950 CATCTACCTGAACATCCAGAGGCGGACCGGCTCCG 985

## RESULT 11

US-09-165-543-1  
; Sequence 1, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP



Db 838 CAGCTCCATCCCGAGGGCACTGCTATGCCGAGTCTTCTTACAACTGGTACTTCTCAT 897  
QY 534 CATTACAAATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGCGCTTATTCAATGTACA 593  
Db 898 CAGGCTCCACCCCTGGAGTCTTTTACGCCCTTCTCTCAGCGTCACTTCTTTAACTCAG 957  
QY 594 GATTACTGGAGCTGTGGAAAGCTGAGGCTCTCAG 629  
Db 958 CATCTACCTGAACATCCAGAGCGCACCGCCTCCG 993

## RESULT 13

US-09-642-855-5  
; Sequence 5, Application US/09642855  
; Patent No. 6413743  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: JMW  
; CURRENT APPLICATION NUMBER: US/09/642,855  
; CURRENT FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 09/167,354  
; PRIOR FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 2699  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CDNA  
US-09-642-855-5

Query Match 11.9%; Score 140.4; DB 4; Length 2699;  
Best Local Similarity 53.6%; Pred. No. 3.5e-34;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;  
QY 3 GTGGAGTCTAACAGTACTGGCATCTTTGCCACCACTGCTCAGTCCCTTGGCATTTT 62  
Db 358 GCGGCGCGCGCGCGCGCGCTTCTCGGACGCTGGACCGCGTGTGGCGCGCT 417  
QY 63 AATGCTCTTCAATTTGCCCTTGTCTAATAGTAGGAATGCTGTGTCTATCTTGGCTTTGT 122  
Db 418 CATGGCGCTGCTCATGCTGGCCACGGTGTGGGCAACGCGTGTCTATGCTCGCTTCGT 477  
QY 123 GGTGGACAGAACTTTAGACATCGAAGTAATTTTCTTAAATTTGGCTATTCTGA 182  
Db 478 GCGCGACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCCGA 537  
QY 183 CTTCCTGTGGGTTGATTTCCATCTCTGTATACCTCCCTCAGCTGTG---TTTAACTG 239  
Db 538 CTTCCTGTGGGCGCTTCTGCTATCCACTGTATGATACCTACCTGCTGACAGCGCGTG 597  
QY 240 GAATTTTGAAGTGAATCTGATGTTTGGCTCATCTAGCTATCTTTTGTGCAACCGC 299  
Db 598 GACCTTGGCGCGCGCGCTTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGTGTGCACTC 657  
QY 300 ATCTGTCTACAATATTGTCTCTATAGTACGATACGATACGATGCTGCTTCAATGCTGT 359  
Db 658 CTCTGCTTCAACATCGTCTCATAGCTACGACCGCTTCTCTGCTGCTACCGAGCGGT 717  
QY 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTGCTCAAAATGGTCTGTTG 419  
Db 718 CTCATACCGGCGCGCGCGCTTCTGCTATGAGTGTGCTGCTGCTGCTGCTGCTG 777  
QY 420 GATACCTGCTTCTTCTGTAATGGCCCGGAGTATCTGGCTTCAGAT-----TCTTGGAA 473  
Db 778 GGTGCTGGCGCTTCTCTGCTGTACGGACGACCATCTCTGAGTGGGAGTACCTGTCCGCGG 837

QY 474 GAACAGCAGAAACAAAGGACTGTGAGCTTGGCTTTGTATACAGAGTGGTATACCTCAG 533  
Db 838 CAGCTCCATCCCGAGGGCACTGCTATGCCGAGTCTTCTTACAACTGGTACTTCTCAT 897  
QY 534 CATTACAAATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGCGCTTATTCAATGTACA 593  
Db 898 CAGGCTTCCACCCCTGGAGTCTTTTACGCCCTTCTCTCAGCGTCACTTCTTTAACTCAG 957  
QY 594 GATTACTGGAGCTGTGGAAAGCTGAGGCTCTCAG 629  
Db 958 CATCTACCTGAACATCCAGAGCGCACCGCCTCCG 993

## RESULT 14

US-09-642-514-5  
; Sequence 5, Application US/09642514  
; Patent No. 6437100  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: ORTI290  
; CURRENT APPLICATION NUMBER: US/09/642,514  
; CURRENT FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: US 09/167,354  
; PRIOR FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 2699  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CDNA  
US-09-642-514-5

Query Match 11.9%; Score 140.4; DB 4; Length 2699;  
Best Local Similarity 53.6%; Pred. No. 3.5e-34;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;  
QY 3 GTGGAGTCTAACAGTACTGGCATCTTTGCCACCACTGCTCAGTCCCTTGGCATTTT 62  
Db 358 GCGGCGCGCGCGCGCGCGCTTCTCGGACGCTGGACCGCGTGTGGCGCGCT 417  
QY 63 AATGCTCTTCAATTTGCCCTTGTCTAATAGTAGGAATGCTGTGTCTATCTTGGCTTTGT 122  
Db 418 CATGGCGCTGCTCATGCTGGCCACGGTGTGGGCAACGCGTGTCTATGCTCGCTTCGT 477  
QY 123 GGTGGACAGAACTTTAGACATCGAAGTAATTTTCTTAAATTTGGCTATTCTGA 182  
Db 478 GCGCGACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCCGA 537  
QY 183 CTTCCTGTGGGTTGATTTCCATCTCTGTATACCTCCCTCAGCTGTG---TTTAACTG 239  
Db 538 CTTCCTGTGGGCGCTTCTGCTATCCACTGTATGATACCTACCTGCTGACAGCGCGTG 597  
QY 240 GAATTTTGAAGTGAATCTGATGTTTGGCTCATCTAGCTATCTTTTGTGCAACCGC 299  
Db 598 GACCTTGGCGCGCGCGCTTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGTGTGCACTC 657  
QY 300 ATCTGTCTACAATATTGTCTCTATAGTACGATACGATACGATGCTGCTTCAATGCTGT 359  
Db 658 CTCTGCTTCAACATCGTCTCATAGCTACGACCGCTTCTCTGCTGCTACCGAGCGGT 717  
QY 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTGCTCAAAATGGTCTGTTG 419  
Db 718 CTCATACCGGCGCGCGCGCTTCTGCTATGAGTGTGCTGCTGCTGCTGCTGCTG 777  
QY 420 GATACCTGCTTCTTCTGTAATGGCCCGGAGTATCTGGCTTCAGAT-----TCTTGGAA 473

**us-10-626-445-5.rni**

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Qy	418	TGGATACTGGCTTCTTGTTGTTAAATGGCCCGATGATTCCTGGCTTCAGA-----TTCCTGG	471
Db	229	TGGGTGCTGGCTTCTCTGCTGTATGGGCGCTGCCATCTTGAGTTGGGAGTACCTGCTGCT	288
Qy	472	AAGAACAGCAGCAACACAAAGGACTGTGAGGCTGGCTTTGTTACAGATGGTGACATCTC	531
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Qy	532	ACCATTCAAATGCTCTTGGAAATTCCTGCTTCCTGTGCATCTCTGTGGCTTAATTCAAATGTA	591
Db	349	ATCTCGGCTCCACCTTCGAGTCTTTCACGGCCCTCCTCAGGTTACCTTCTTCAACCTC	408
Qy	592	CAGATTACTGGAGCCTGTGGAAGCGTA	619
Db	409	AGCATCTACCTGAACATCCAGAGCGCA	436

Search completed: October 1, 2004, 13:54:38  
Job time : 115 secs

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2	686.6	58.4	1173	9	US-09-910-411-1	Sequence 1, Appli
3	686.6	58.4	1173	13	US-10-349-253A-1	Sequence 1, Appli
4	686.6	58.4	1173	13	US-09-875-076-13	Sequence 13, Appli
5	686.6	58.4	1173	13	US-09-876-252-13	Sequence 13, Appli
6	686.6	58.4	1173	14	US-10-052-193-1	Sequence 1, Appli
7	686.6	58.4	1173	15	US-10-272-983-13	Sequence 13, Appli
8	686.6	58.4	1173	15	US-10-354-769-1	Sequence 1, Appli
9	686.6	58.4	1173	15	US-10-393-807-13	Sequence 13, Appli
10	686.6	58.4	1173	16	US-10-417-820A-13	Sequence 13, Appli
11	686.6	58.4	1173	17	US-10-723-955-13	Sequence 13, Appli
12	686.6	58.4	1173	17	US-10-737-619-1	Sequence 1, Appli
13	686.6	58.4	1173	17	US-10-782-596-13	Sequence 13, Appli
14	686.6	58.4	1266	10	US-09-891-138A-5	Sequence 5, Appli

QY	121	GTGGTGGACAGAAACCTTAGACATCGAAGTAATATATTTTTTTCTTAATTTGGCTATTCT	180
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QY	121	GTGGTGGACAAAAACCTTAGACATCGAAGTAGTATATTTTTTTCTTAACCTTGGCCATCTCT	180
Db	121		
QY	181	GACTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGTGTGTTTAACTGG	240
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QY	181	GACTTCCTTGTGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTGGAATGG	240
Db	181		
QY	241	AATTTTGGAAAGTGGAAATCTGCATATGTTGGCTCATCTACTGACTATCTTTTGTGCACCGCA	300
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QY	241	GAATTTTGGAAAGAAATCTGTGTATTTTGGCTCAGTACTGACTATCTGTATGTATACGCA	300
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QY	301	TCCTGTCTACAAATATGTCTCATTTAGCTACGATCGATCCAGTCTAGTCTCAAAATGCTGTG	360
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QY	301	TCCTGTATATAACATTTGTCCTCATCAGCTATGATCGATACCTGTCAATGCTCAATGCTGTG	360
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QY	901	AGGAAGCTAGCCAGGTCATCTGGCCATCTCTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA	960
Db	895	AGGAGATTAGCCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTTTGCTGGGCTCCA	954
QY	961	TACTGTCTGTTCAAAATTTGCTTTCAACTTACCCAGAACGGAACGCCCAATCGGTG	1020
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QY	1021	TGGTACAGATTTGCTCTTGGCTGCAATGGTTTCAATTCGTTTGTATTAATCCCTTTCTGTAC	1080
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Db	1075	CCATTTGTGCACAGCGCTTTCCAAAAGGCTTTCTTTGAAAATATTTTGTATATAAAAGCAA	1134
QY	1141	CCAGCGCTGTCAAGAAC---CAGTCAGTATCTTCTTGA	1176
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RESULT 2
US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derek
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-910-411-1

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QY 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGGCCCTAGCCATGCTGGATTCTCCACT 660  
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QY 595 TGGAGCCTGTGGAAGCGTAGCATCTCAGTAGGTGGCCAAAGCCATCTCTGGAGTCACTGCT 654  
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QY 661 ACCCTCTCCAGTGTCTCAGGACACTTACACAGAGCTGGGTGGCTTGCAGGACAAAGTAAT 720  
Db |||||  
QY 655 GTCTCTCCACATCTGTGGACACTCATTCAGAGTAGACTATCTTCAAGGAGATCTCTT 714  
Db |||||  
QY 721 CTTGGATTGAAGGAATCAGCTGTCATCTCGTCACTCAGAAAGTCCTCGAAGAAAGAGCAGC 780  
Db |||||  
QY 715 TCTGCATCGACAGAAGTCTCTGTCATCTCTTCAATTCAGAGACACAGAGGAAAGAGTAGT 774  
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QY 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGTTC 834  
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QY 835 TTTCTCCCAATCAGATTCTGTAGCTTCTACCAAAGGGAACATGTTGAACCTGCTTAGAGCC 894  
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QY 1015 TGGTATAGAAATGCAATTTGGCTTCACTGGTTCAGTGGTTCAATTCCTTGTCAATCCTTTTGTAT 1074  
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QY 1135 CCTCTACCATCAACACACAGTCGGTCAGTATCTTTTAA 1173  
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## RESULT 3

US-10-349-253A-1  
; Sequence 1, Application US/10349253A  
; Publication No. US20040043393A1  
; GENERAL INFORMATION:  
; APPLICANT: Aubart, Kelly  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Fitzgerald, Laura  
; APPLICANT: Graybill, Todd  
; APPLICANT: Li, Xiatong  
; APPLICANT: Michalovich, David  
; APPLICANT: Morrow, Dwight  
; APPLICANT: Zhu, Yuan  
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor  
; FILE REFERENCE: GP70655-2C2  
; CURRENT APPLICATION NUMBER: US/10/349,253A  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 09/910,411  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: 09/693,761  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/497,790  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/431,898  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-349-253A-1

Query Match 58.4%; Score 686.6; DB 13; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 2e-209;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
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QY 1 ATGCCAGATCTAATAGCACATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
Db |||||  
QY 61 TTAATGTCTTCAATTTGGCTTTTGTCTAATAGTAGCAATGCTGTGGTCACTCTTAAAGCCTTT 120  
Db |||||  
QY 61 TTTATGTCTTCTAGTAGCTTTTGTCTAATAGTAGCAATGCTGTGGTCACTCTTAAAGCCTTT 120  
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QY 241 AATTTGGAAGTGGAAATCTGCAATTTTGGCTCATTTACTGACTATCTTTTGTGACCGCA 300  
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QY 241 GATTTGGAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300  
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QY 301 TCTGTCTTACAATATTGTCCTCATTTAGCTACGATCGATACAGTCAGTTCCTCAATTTGCTG 360  
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QY 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTCAGTCTCAATTTGCTG 360  
Db |||||  
QY 361 TCTTATAGGCTCAACACACTGTCATCATGAAGATTGTTGCTCAATTTGCTGCTGTTTGG 420  
Db |||||  
QY 361 TCTTATAGAACTCAACATCTGGGGTCTTGAAGATTGTTACTCTGATGTTGGGCTTTGG 420  
Db |||||  
QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTCTTCTGGAAGAACAGC 480  
Db |||||  
QY 421 GTGCTGGCTTCTTCTAGTGAATGGCCAAATGATTTCTAGTTTCAGAGTCTTGAAGAA--- 476  
Db |||||  
QY 481 ACGAACACAAAGACTGTGAGCCTGCTTTGTGTACAGAGTGGTACATCTCCATTTACATTA 540  
Db |||||  
QY 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTGCTCATCA 534  
Db |||||  
QY 541 ATGCTCTTGGAAATTCCTGCTTCTCTGTCATCTCTGTTGGCTTATTTCAATGTACAGATTAC 600  
Db |||||  
QY 535 TCATTTCTTGGAAATTCGTGATCCAGTCATCTTAGTCGCTTATTTCAACATGAATTTAT 594  
Db |||||  
QY 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGTGCCCTAGCCATCTCGATTTCTCCACT 660  
Db |||||  
QY 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGTGCCAAAGCCATCTCTGAGCTGATGCT 654  
Db |||||  
QY 661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGTGGGTGGCTTGCAGGACAAAGTAAT 720  
Db |||||  
QY 655 GTCTCTTCCACATCTGTGGACACTCATTCAGAGTAGACTATCTTCAAGGAGATCTCTT 714  
Db |||||  
QY 721 CTTGGATTGAAGGAATCAGCTGTCATCTCGTCACTCAGAAAGTCCTCGAAGAAAGAGCAGC 780  
Db |||||  
QY 715 TCTGCATCGACAGAAGTCTCTGTCATCTCTTCAATTCAGAGACACAGAGGAAAGAGTAGT 774  
Db |||||  
QY 781 ATCTGTGTCTTAAAGACTCACATGAACAGCAGTATCACTGCTTCAAGTGGGTTCC 840  
Db |||||  
QY 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGGTTCC 834  
Db |||||  
QY 841 TTTCTGGCGATCGGAAGGTGAGCGCTTCGCCAAAGGGAGTAGCAGAGCTTCTCAGAGGC 900  
Db |||||  
QY 835 TTTCTCCCAATCAGATTCTGTAGCTTCTACCAAAGGGAACATGTTGAACCTGCTTAGAGCC 894  
Db |||||  
QY 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960  
Db |||||  
QY 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTGCTGTGCTGGGCTCCA 954  
Db |||||  
QY 961 TACTGTCTGTTCACAATGTCTTTCACTTTACCCAGAACGGAAACGCCCAAAATCGGTG 1020  
Db |||||  
QY 955 TATTCTCTGTTCACAATGTCTTCAATTTATTTCTCTCAGCAACAGGCTCTTAATCAGTT 1014  
Db |||||



Db 955 TATTCTCTGTTCAAAATGTCCTTTCAATTTATTCTCAGCAACAGGTCCTAAATCAAGTT 1014  
QY 1021 TGGTACAGATGCTCTGGCTGCAATGGTTCAATTCGTTGTAATCCCTTTCTGTAC 1080  
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCAATTCCTTTGTCATTCCTTTTGTAT 1074  
QY 1081 CCTTGTGTACAGGCTTTCCAGAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140  
Db 1075 CCAATGTGTCAAGAGCGCTTTCAAAGGCTTTCTTGAAATATTTGTATATAAAGCAA 1134  
QY 1141 CCAGCGGTGTACAGAAC--CAGTCAGTATCTTCTTGA 1176  
Db 1135 CCTTACCATCAACACAGTCGGTCAGTATCTTCTTAA 1173

RESULT 5  
US-09-876-252-13  
; Sequence 13, Application US/09876252  
; Publication No. US20030018182A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Re  
; FILE REFERENCE: AREN-0054  
; CURRENT APPLICATION NUMBER: US/09/876,252  
; CURRENT FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/152,524  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/151,114  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/108,029  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,127  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/141,448

; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/156,555  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,634  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,653  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/157,280  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,281  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/156,633  
; NUMBER OF SEQ ID NOS: 146  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-876-252-13

Query Match 58.4%; Score 686.6; DB 13; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 2e-209;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAAACAGTACTGGCATCTTGCACACAGTGTCTCAGGTCCCTTTGGCATTT 60  
Db 1 ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
QY 61 TTAATGCTCTTCAATTTGCCCTTTGCTATAATGGTAGGCAATGCTGTGGTCATCTTAGCCTTT 120  
Db 61 TTTATGTCCTTAGTAGCTTTTGCTATAATGCTAGGAAATGCTTTGGTCATCTTTAGCCTTT 120  
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAGTAATTTTCTTAATTTGGCTATTTCT 180  
Db 121 GTGGTGACAGAAACCTTAGACATCGAAGTAGTAATTTTCTTAATTTGGCTATTTCT 180  
QY 181 GACTTCCTCGTGGTTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTGTTAACTGG 240  
Db 181 GACTTCCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCAGCTGTGTGTTAACTGG 240  
QY 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATCTACTGACTATCTTTTGGCACCGCA 300  
Db 241 GATTTTGGAAAGAAATCTGTGTAATTTTGGCTCATCTACTGACTATCTTTTATGTACAGCA 300  
QY 301 TCTGTCTACAATPATTTGTCCTCAATAGCTACGATCCGATCCAGTCCAGTGTTCAAATGCTGG 360  
Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTGCTAGTCTCAATGCTGG 360  
QY 361 TCTTATAGGCTCAACACACTGGCAATGAGAGATTGTTGTCTCAAAATGCTGGCTGTTGG 420  
Db 361 TCTTATAGAACTCAACATACTGGGTCTTGAAGATTGTTACTCTCATGCTGGTGGCCGTTGG 420  
QY 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGTTCTGGCTTCAGATCTTCAGATCTTGGAAAGACG 480  
Db 421 GTGCTGGCTTTCTTAGTGAATGGGCCAAATGTTCTAGTTTCAGAGTCTTTGAAAGGA---- 476  
QY 481 ACGAACACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGTGTACATCTCCTCACCATTACA 540  
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTGTTTTCGGAAATGGTATCATCTTGGCCATACA 534  
QY 541 ATGCTTTTGGAAATTCCTGCTTCTGTCTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600  
Db 535 TCATTTCTTGAATTCGTGATCCAGTCCATCTTAGTGGCTTATTTCAACATGAATATTAT 594  
QY 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGGCCCTAGCCATGCTGGATTCTTCACT 660

595	Db	TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAGGCCATCCTGGACTGCTCT	654
661	Qy	ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGTGGCTTGCAGGACAAATAAT	720
655	Db	GTCTCTTCCAAATCTGTGACACTCATCTCAGAGGTAGACTATCTTCAAGGAGATCTCTT	714
721	Qy	CCTGGATTGAAGGAATCAGTGTGATCTGTCATCTCAGAAAGTCTCGAAGAAAGACGAC	780
715	Db	TCTGATCGACAGAGTTCCTGATCCTTTCATCTCAGAGACAGAGGAGAAAGTAGT	774
781	Qy	ATCCTGTGTCTTAAAGACTCAGATCAACAGAGAGTATCACTGCTTCAAAGTGGGTTC	840
775	Db	CTCATGTTTTCCCTCAAGAACCAAGTGAATGAAATGGTTCAGAACTGCTTAGAGCC	834
841	Qy	TTCTGGCGATCGAAGATGCGAGCGCTTCCGCAAGGAGTACGACAGCTTCTCAGAGGC	900
835	Db	TTCTCCCAATCAGATTCCTGATCCTTTCATCTCAGAGACAGAGTCTTGAATGCTTAGAGCC	894
901	Qy	AGGAAGCTAGCCAGTCACTGGGCATCTTCTCAGAGCGCTTTCGCAATTTGCTGGGTCCA	960
895	Db	AGGAGATTAGCCAACTCAGTGGCAATCTCTTAGGGGTTTTTGTGTTTCTGGGTCCA	954
961	Qy	TACTGTCTGTTCACAAATGTCTTCAACTTACCCAGACGGAAGCCCAATCGGTG	1020
955	Db	TATTCTCTGTTCACAAATGTCTTTCATTTTATCTCAGCAACAGAGTCTTAAATCAGTT	1014
1021	Qy	TGGTACAGCATTCGCTTCTGCTCAATGGTTTCAATTCGTTTGTAAATCCCTTTCTGTAC	1080
1015	Db	TGGTATAGAAATGTGATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTGTAT	1074
1081	Qy	CCTTTGTCTCAGCGGTTTCCAGAAAGCTTTCTGGAAGTACTTTGTGTGACAAAGCAA	1140
1075	Db	CAATGTGTCAAGCGCTTTCAAAAGGCTTTCTTTGAAATATTTTGTATATAAAAAGCAA	1134
1141	Qy	CAAGCGTGTCAAGAAC---CAGTCAGTATCTTTTGA 1176	
1135	Db	CCTCTACCATCAACACACAGTCGGTCAGTATCTTTCTTAA 1173	
RESULT 7			
US-10-272-983-13			

595	Db	TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAGGCCATCCTGGACTGCTCT	654
661	Qy	ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGTGGCTTGCAGGACAAATAAT	720
655	Db	GTCTCTTCCAAATCTGTGACACTCATCTCAGAGGTAGACTATCTTCAAGGAGATCTCTT	714
721	Qy	CCTGGATTGAAGGAATCAGTGTGATCTGTCATCTCAGAAAGTCTCGAAGAAAGACGAC	780
715	Db	TCTGATCGACAGAGTTCCTGATCCTTTCATCTCAGAGACAGAGGAGAAAGTAGT	774
781	Qy	ATCCTGTGTCTTAAAGACTCAGATCAACAGAGAGTATCACTGCTTCAAAGTGGGTTC	840
775	Db	CTCATGTTTTCCCTCAAGAACCAAGTGAATGAAATGGTTCAGAACTGCTTAGAGCC	834
841	Qy	TTCTGGCGATCGAAGATGCGAGCGCTTCCGCAAGGAGTACGACAGCTTCTCAGAGGC	900
835	Db	TTCTCCCAATCAGATTCCTGATCCTTTCATCTCAGAGACAGAGTCTTGAATGCTTAGAGCC	894
901	Qy	AGGAAGCTAGCCAGTCACTGGGCATCTTCTCAGAGCGCTTTCGCAATTTGCTGGGTCCA	960
895	Db	AGGAGATTAGCCAACTCAGTGGCAATCTCTTAGGGGTTTTTGTGTTTCTGGGTCCA	954
961	Qy	TACTGTCTGTTCACAAATGTCTTCAACTTACCCAGACGGAAGCCCAATCGGTG	1020
955	Db	TATTCTCTGTTCACAAATGTCTTTCATTTTATCTCAGCAACAGAGTCTTAAATCAGTT	1014
1021	Qy	TGGTACAGCATTCGCTTCTGCTCAATGGTTTCAATTCGTTTGTAAATCCCTTTCTGTAC	1080
1015	Db	TGGTATAGAAATGTGATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTGTAT	1074
1081	Qy	CCTTTGTCTCAGCGGTTTCCAGAAAGCTTTCTGGAAGTACTTTGTGTGACAAAGCAA	1140
1075	Db	CAATGTGTCAAGCGCTTTCAAAAGGCTTTCTTTGAAATATTTTGTATATAAAAAGCAA	1134
1141	Qy	CAAGCGTGTCAAGAAC---CAGTCAGTATCTTTTGA 1176	
1135	Db	CCTCTACCATCAACACAGTCGGTCAGTATCTTTCTTAA 1173	
RESULT 6			
US-10-052-193-1			
; Sequence 1, Application US/10052193			
; Publication No. US20020132755A1			
; GENERAL INFORMATION:			
; APPLICANT: Pfizer, Inc.			
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS			
; FILE REFERENCE: PC10963A			
; CURRENT APPLICATION NUMBER: US/10/052,193			
; CURRENT FILING DATE: 2002-01-17			
; PRIOR APPLICATION NUMBER: 0101223.6			
; PRIOR FILING DATE: 2001-01-17			
; NUMBER OF SEQ ID NOS: 10			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 1173			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-052-193-1			
Query Match 58.4%; Score 686.6; DB 14; Length 1173;			
Best Local Similarity 75.1%; Pred. No. 2e-209;			
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;			
Qy	1	ATGTCGAGTCTAACAGTACTGCGATCTTGGCCACCAGTGTCTCAGGTCCCTTGGCATTT	60
Db	1	ATGCCAGATCTAATAGCAATCAATTTATCATCTAAGCACTCGTGTACTTTAGCAATTT	60
Qy	61	TTAATGCTTCATTTGGCTTGTCTAATAGTGGTCAATGCTGTGTCATCTTAGCCTTT	120
Db	61	TTTATGTCTTAGTAGCTTTTGTCTAATAGCTAGGAATGCTTTGGTCATTTTAGCTTTT	120
Qy	121	GTGGTGGACAGAACCTTAGACATCGAAGTAAATATTTTTTCTTAAATTTGGCTATTTCT	180

RESULT 7  
US-10-272-983-13

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; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-272-983-13

Query Match      58.4%; Score 686.6; DB 15; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTCCACCAGCTGCTCAGTCCCTTGGCATTT 60
DB 1 ATGCCAGATCTAATAGCACAATCAATTATCTACTAGACACTGCTGTTACTTTAGCATTT 60
QY 61 TTAATGCTTTCATTGCGCTTTGTCTATAAAGGTAGGCAATGCTGTGTCATCTTTAGCCTTT 120
DB 61 TTTATGCTCCTTAGTAGCTTTTGTCTATAAATGCTAGGAAATGCTTTGGTCACTTTAGCTTTT 120
QY 121 GTGGTGCAGACAACCTTAGACATCGAAGTAATTATTTTCTTAATTGGCTATTCT 180
DB 121 GTGGTGCAGACAACCTTAGACATCGAAGTAGTATTATTTTCTTAATTGGCCATCTCT 180
QY 181 GACTTCTCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
DB 181 GACTTCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 241 AANTTTGGAAGTGGAAATCTGCAATGTTTTGGCTCACTACTGACTATCTTTTGTGCAACGCA 300
DB 241 GATTTTGGAAAGGAATCTGTGTAATTTGGCTCACTACTGACTATCTGTTAATGACAGCA 300
QY 301 TCTGCTCAATATCTCTCTCATTAGCTAGGATCGATACAGTCACTGTTCAATGCTGTG 360
DB 301 TCTGTATATAACATGCTCTCTCACTAGCTATGATCGATACCTGTCACTCTCAATGCTGTG 360
QY 361 TCTTATAGGCTCAACACACTGSCATCATGAGATTGTTGCTCAATGCTGCTGTTTGG 420
DB 361 TCTTATAGACTCAACATCTGGGTCTTGAAGATTGTTTACTCTGATGTCGCGCTTGG 420
QY 421 ATACTGGCTTTCTTGTGTAATGGCCGATGATTCTGGCTTCAGATTCTTTGGAAGAACAGC 480
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Db 421 GTGCTGGCCTTCTTAGTGAATGGCCCAATGATTCTAGTTTCAGAGTCTTTGAAGGA----- 476
QY 481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTCTTTTTCGGAATGTTACATCTTGGCCATACA 534
QY 541 ATGCTCTTGGAAATTCCTGCTTCCCTGTCATCTCTGCTGGCTTATTTCAATGTACAGATTAC 600
Db 535 TCATTCTTGGAAATTCGTTGATCCCACTGATCTTAGTCTGCTTATTTCAACATGAATATTAT 594
QY 601 TGGAGCCTGTGGAGAGCGTAGGGCTCTCAGTAGTGCCCTAGCCATCTGGATTCTCCACT 660
Db 595 TGGAGCCTGTGGAGAGCGTAGTATCTCAGTAGTGCCCAAGCCATCTGGACTGACTGCT 654
QY 661 ACTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGTGGCTTGCAGGACAAAGTAAT 720
Db 655 GTCTCTTCCAACTCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 721 CCTGGATTGAAGNATCAGTGTGATCTGCTCACTCAGAAAGTCTCTCGAAGAAAGAGCAGC 780
Db 715 TCTGCATCGACAGAAAGTTCTGCTATCCTTTCAATTCAGAGAGACAGAGGAGAAAGTAGT 774
QY 781 ATCTGTGTGCTCTTAAGGACTTCATGAACAGAGATATCACTGCTTCAAGTGGTTC 840
Db 775 CTGATGTTTCTTCAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGGTTC 834
QY 841 TTTGCGCATCGGAAAGTGCAGCGCTTCGCCAAGGGAGTACGACAGAGCTTCTCAGAGGC 900
Db 835 TTTCCCAATCAGATTCTGTAGCTTTTCAACAAAGGGAACATGTTGAATGCTTAGAGCC 894
QY 901 AGAAGCTAGCCAGGTCACTGGCCATCTTCTCAGGCGCTTTTGCATTTGCTGGGTCCA 960
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTTCTTAGGGGTTTTTGTGCTTTGCTGGGTCCA 954
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Db 955 TATTCTCTGTTCACAATTTGCTTTCAATTTATCTCAGCAACAGGTCTCAATCAAGT 1014
QY 1021 TGCTACAGCATTCCTTCTGGCTGCAATGTTCAATTTGTTTGTATTCCTTCTTGTATC 1080
Db 1015 TGGTATAGAATTGCAATTTTGGCTTCACTGTTGTTCAATTTCTTGTCAATCTCTTTGTAT 1074
QY 1081 CCTTGTGTACAGGCGTTTCAGAAAGGCTTTCAGAAAGTCTTCTGGAAGATCTTTGTGCAAAAGCAA 1140
Db 1075 CCATTGTGTACAGGCGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAA 1134
QY 1141 CCAGCGCTGTTCAGAAAC--CAGTCAAGTATCTTCTTGA 1176
Db 1135 CCTCTACCATCAACACAGTGGTCAAGTATCTTCTTAA 1173

RESULT 8
US-10-354-769-1
; Sequence 1, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1

Query Match      58.4%; Score 686.6; DB 15; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGGCACCAGCTGCTCAGGTCCTCCCTTGGCAATTT 60
Db 1 ATGCGAGATCTAATAGACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
QY 61 TTAATGCTTCAATTTGCTTATTAATAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 TTTATGCTTCTAGTCTTTGCTATATATGCTAGGAATGCTTTGGTCAATTTTATGCTTTT 120
QY 121 GTGCTGGACAGAACTTAGACATCGAAGTAATTTTCTTAAATTTGGCTATTTCT 180
Db 121 GTGCTGGACAGAACTTAGACATCGAAGTAATTTTCTTAAATTTGGCTATTTCT 180
QY 181 GACTTCTCTGCTGGGTGTTGATTTCCATTCCTCTGTACATCCCTCAGTGTGTTTAACTGG 240
Db 181 GACTTCTTGTGGGTGCTGATCTCCATTCCTTGTATACATCCCTCAGTGTGTTTAACTGG 240
QY 241 AATTTGGAAGTGAATCTGATGATTTTGGCTCATTACTGACTATCTTGTGACCCGA 300
Db 241 GATTTTGAAGGAATCTGTGATTTTGGCTCATTACTGACTATCTTGTGACACGA 300
QY 301 TCTGCTACATATTGCTCTCATTTAGCTAGCATGATGATGATGATGATGATGATGATGATG 360
Db 301 TCTGATATATCAATGCTCTCATTTAGCTAGCATGATGATGATGATGATGATGATGATG 360
QY 361 TCTTATAGAGCTCAACACTGCTGGGTCTTGAAGATTTGTTACTCTGATGCTGGCGCTTGG 420
Db 361 TCTTATAGAGCTCAACACTGCTGGGTCTTGAAGATTTGTTACTCTGATGCTGGCGCTTGG 420
QY 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTTGGCTTCAATGCTGCTGCTGCTGCTGCTG 480
Db 421 GTGCTGGCTTCTTGGTAAATGGCCGATGATTTGGCTTCAATGCTGCTGCTGCTGCTGCTG 480
QY 481 ACGAACACAAAGACTGTGAGCTGCTGCTTGTATACAGAGTGTGATCACTCTCCACCAATACA 540
Db 477 --TGAAGTGTGAATGTGAACCTGGAATTTTTCGAATGATGATCACTCTTGGCATCACA 534
QY 541 ATGCTCTTGGAAATTCCTGCTCTCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 535 TCATTTCTTGGAAATTCCTGCTCTCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 594
QY 601 TGGAGCTGTGGAAGGTAGGCTCTCAGTAGTGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 595 TGGAGCTGTGGAAGGTAGGCTCTCAGTAGTGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 654
QY 661 ACTCTTCCAGTCTTCCAGACACTTACACAGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 655 GTCTCTTCCAGTCTTCCAGACACTTACACAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 714
QY 721 CCTGGAATGAAGGAATFAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 715 TCTGCTATCAGACAAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774
QY 781 ATCTGCTGCTGCTTAAAGTCTACATGAACAGAGTATCACTGCTTCAAGTGGGCTTCC 840
Db 775 CTGATGCTTCTTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTCC 834
QY 841 TCTGCGATCGGAAAGTGCAGGCTTTCGCAAGGAGTACGACAGAGTCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATCTGTAGTCTTTCACCAAGGGAACATGTTGAATGCTGTAGAGCC 894
QY 901 AGGAAGCTACGCCAGGTCACTGGCCATCTTCTGAGGCTTTTCTGAGGCTTTTCTGCTGGCTCCA 960

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Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGCTCCA 954
QY 961 TACTGTCTGTTCAAAATTTGCTTTTCAACTTACCCAGAACGCGCCCAAAATGCGGTG 1020
Db 955 TATTTCTGTTCAAAATTTGCTTTTCAACTTATTTTCTCAGCAACAGGCTCTAAATCAGTT 1014
QY 1021 TGGTACAGCATTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1015 TGGTATAGAAATTCGATTTTGGCTTTCAGTGGTTCAAATTTTCTTGTCAATCTCTTTGTAT 1074
QY 1081 CTTTGTGCTACAGGCTTTTCCAGAGGCTTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140
Db 1075 CCATTTGTGCTACAGGCTTTTCCAGAGGCTTTCTGGAAGATACCTTTGTGTGATATAAAGCAA 1134
QY 1141 CCAGCGCTGCTCACAGAAC--CAGTCACTGATCTCTTTGGA 1176
Db 1135 CCTTACCATCACACACAGCTCGTCACTGATCTCTTTAA 1173

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RESULT 9
US-10-393-807-13
; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-393-807-13

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Query Match      58.4%; Score 686.6; DB 15; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGGCACCAGCTGCTCAGGTCCTCCCTTGGCAATTT 60
Db 1 ATGCGAGATCTAATAGACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
QY 61 TTAATGCTTCAATTTGCTTATTAATAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 TTTATGCTTCTAGTCTTTGCTATATATGCTAGGAATGCTTTGGTCAATTTTATGCTTTT 120

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121 GTGTGGCAGAGAAACCTTAGACATCGAAGTAATATATTTTCTTAATTTGGCTATTCT 180  
121 GTGTGGCAGAGAAACCTTAGACATCGAAGTAGTATATTTTCTTAATTTGGCCTCTCT 180  
181 GACTTCCTCGTGGTGTGATTTCCATTCCTCTGTACATCCCTACGCTGTGTTAACTGG 240  
181 GACTTCCTCGTGGTGTGATTCCTCATTCCTTTGTACATCCCTCACACGCTGTTGGAATGG 240  
241 AATTTTGGAGTGGAACTGTCATGTTTGGCTCATTAATGACTATCTTTTGTGCAACGCA 300  
241 GATTTTGGAGAAAGAAATCTGTGTAATTTGGCTCACTACTGACTATCTGTATGTACAGCA 300  
301 TCTGTCTPACAAATATGTCTCATTAGCTACGATCAGATACCAGTCAGTTCCTCAAAATGCTGTG 360  
301 TCTGTATATAACATTTGCTCATCAGCTATGATGATACCTGTGTCAGTCTCAAAATGCTGTG 360  
361 TCTATAGGCTCAACACATCGGATCATGAAGATTTGCTCAAAATGCTGTGTTGG 420  
361 TCTATAGAACTCAACATCTGGGCTCTTGAAGATTTGCTCAAAATGCTGTGTTGG 420  
421 ATACTGGCTTCTTGTGTAATGGCCGATGATCTGGCTTCAGATTTCTTGGAAAGCAGC 480  
421 GTGTGCGCTTCTTAGTGAATGGCCCAATGATCTAGTTTCAGAGTCTTGGAAAGGA---- 476  
481 ACGAACAACAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCTCTCAACATTACA 540  
477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTGCCATCACA 534  
541 ATGCTCTTGAATTCCTGCTCTCTGTCATCTCTGTGGCTTATTTCAATGACAGATTAC 600  
535 TCATCTTGAATTCGATGCCAGTCATCTTAGTCTGCTTATTTCAACATGAATATTTAT 594  
601 TGGAGCTGTGGAAGGCTAGGCTCTCAGTAGTGCCCTAGGATCGCTGCTGATTTCTCCACT 660  
595 TGGAGCTGTGGAAGGCTAGGCTCTCAGTAGTGCCCTAGGATCGCTGCTGATTTCTCCACT 654  
661 ACCTCTTCCAGTCTTTCAGGACATTTACACAGAGTGGGCTGGCTTTCGAGCAAGATTAAT 720  
655 GTCTCTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGATCTCTT 714  
721 CCTGGAATGAGAAATCAGCTGATCTGTCATCTAGAAAGTCTCTGAGAAAGAGCAGC 780  
715 TCTGCAATCAGCAAGTCTCTGCTGATCTCTTCAATTCAGAGAGACAGAGAGAGATAGT 774  
781 ATCTCTGTGCTTAAAGGCTCATCATGAACAGCAGATATCACTGCTTCAAGTGGCTTCC 840  
775 CTCATGTTTCTTCAAGAACCAAGATGATAGCAATACAAATGCTTCCAAATGGGTTC 834  
841 TTCTGGCGATCGGAAAGTGCAGGCTTTCGCCAAAGGAGTACGACAGAGCTTCTCAGAGGC 900  
835 TTCTCCCAATCAGATTTCTGTAGCTTTTCAACAAAGGGAACATGTTGAATGCTTAGAGCC 894  
901 AGGAAGCTAGCAGGTCACTGGCCATCTTCTGAGCGCTTTTGGCAATTTGCTGGGCTCCA 960  
895 AGGAGATTAGCAGGATCACTGGCCATCTTCTTAGGGGTTTTTGTCTGCTGGGCTCCA 954  
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955 TATTCTCTGTTTCAAAATGTGCTTTCAATTTATCTCTCAGCAACAGGCTTAAATCAGTT 1014  
1021 TGGTACAGATTCCTTCTGGCTGCAATGTTTCAATTCGTTTGTATATCCCTTCTCTGTAC 1080  
1015 TGGTATAGAATTCATTTTGGCTTCAAGTGTGTTCAATTCCTTGTCAATCTCTTTGTAT 1074  
1081 CCTTTGTGTACAGGCGTTTCAGAGGCTTTCTGGAAGATATTTTGTGTGACAAAGCAA 1140  
1075 CCATTTGTGTACAGGCGTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAA 1134  
1141 CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTGA 1176  
1135 CCTTACCATTCACACACAGTCGGTCAGTATCTTCTTAA 1173

RESULT 10

US-10-417-820A-13  
; Sequence 13, Application US/10417820A  
; Publication No. US20030229216A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lowitz, Kevin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7 US28 CON  
; CURRENT APPLICATION NUMBER: US/10/417,820A  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; Remaining prior application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13

; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-417-820A-13

Query Match 58.4%; Score 686.6; DB 16; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 2e-209;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTGGAGTCTAAACAGTACTGGCATCTTGGCCACAGCTGCTCAGTCCCTTGGCATTT 60  
DB 1 ATGCCAGATCTAATAGCAATCAATTTATCACTAAGCACCTGTTTACTTTAGCATTT 60  
QY 61 TTAAGTCTTCAATTTGCTTTGCTATAATGTTAGGCAATGCTGTGGTCACTTTAGCCTTT 120  
DB 61 TTATGCTCTAGTAGCTTTTGTATAATGCTAGGAAATGCTTTGCTCAATTTAGCTTT 120  
QY 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATATTTTCTTAATTTGGCTATTTCT 180  
DB 121 GTGTGGACAAACACCTTAGACATCGAAGTAGTATATTTTCTTAACTTGGCATCTCT 180  
QY 181 GACTTCTCGTGGTGTGATTTCCATTCTCTGTACATCCCTCAGCTGTTTAACTCG 240  
DB 181 GACTTCTTGTGGTGTGATCTCCATTTCTTTGTACATCCCTCAGCTGTTTGAATGG 240  
QY 241 AATTTTGGAAAGTGAATCTGCAATGCTGCTATTTTGGCTCAATTAATGACTATCTTTTGTGCAACGCA 300  
DB 241 GATTTTGGAGAAAGAAATCTGTGTAATTTGGCTCACTACTGACTATCTGTATGTACAGCA 300  
QY 301 TCTGTCTCAATATTTGCTCTCTATTTAGCTACGATCGAATACAGTCAAGTTTCAAAATGCTGTG 360  
DB 301 TCTGTATATAACATTTGCTCTCTCATCATGATGATGATGATGATGATGATGATGATGATG 360  
QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGTTGCTCAAAATGGTGGCTTTGG 420

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Db 361 TCCTATAGACTCAACATCTGGGCTCTGAAGATTGTTACTCTGATGGTGGCGTTGG 420
Qy 421 ATATGGCTTTCTTGGTAATATGGCCGAGATCTTGGCTTCAGATTCCTTGAAGAACAGC 480
Db 421 GTGCTGGCTTCTTAGTGAATGGGCAATGATCTTAGTTTCAGAGTCTTGAAGGA---- 476
Qy 481 ACGAACAAAGGACTGTGAGCGTGGCTTCTTACAGAGTGATCATCTCCACCATTACA 540
Db 477 --TGAAGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534
Qy 541 ATGCTCTTGGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Db 535 TCATTTCTTGAATTCGTGATCCAGTCATCTTAGTCTGCTTATTTCAACATGAATATTTAT 594
Qy 601 TGGAGCTGTGGAAGCTGAGGCTCTCAGTAGTGGCTTACGATGCTGGATCTCCACT 660
Db 595 TGGAGCTGTGGAAGCTGAGGCTCTCAGTAGTGGCTTACGATGCTGGATCTCCACT 654
Qy 661 ACCTCTTCCAGTCTCAGGACACTTACACAGAGCTGGGCTTGCAGGACAGTAAT 720
Db 655 GTCTCTTCCACATCTGTGGACATCTATCAGAGTAGACTATCTTCAAGAGATCTCTT 714
Qy 721 CTTGATTTGAAGGATCAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db 715 TCTGATCGACAGAAATCTCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 774
Qy 781 ATCTGCTGTCTTGAAGACTCACATGAACAGCAGTATCAGTCTCTCAAGTGGTTC 840
Db 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGGTTC 834
Qy 841 TTTGGGATCGGAAGTGCAGCGCTTCGCAAGGAGTAGTCAGAGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATCTGTAGTCTTCCACCAAGGACATGTTGAAGTCTTAGAGCC 894
Qy 901 AGAAGCTAGCCAGCTCAGTGGCCATCTCTCTGAGCGCTTTTGGCCATTTGCTGGCTCA 960
Db 895 AGGAGATAGCCAGCTCAGTGGCCATCTCTCTGAGCGCTTTTGGCTGTTTGGTGGCTCCA 954
Qy 961 TACTGTCTGTACAAATTTCTCTTCACTTACCCAGAGCGGAGCGCCCAAAATCGGTG 1020
Db 955 TATTCTCTGTTCACAAATTTCTCTTCAATTTTATCTCTCAGCAACAGGCTCTAAATCAGTT 1014
Qy 1021 TGGTACAGATTCCTCTCTGCTGCAATGGTTCAATTTGTTTAAATCCCTTCTGTAC 1080
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Qy 1081 CTTTGTGTCAAGCGCTTTCAGAGGCTTTCTGGAAGATATCTTGTGTGACAAAGCAA 1140
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Qy 1141 CCAGCGCTGTACAGAAC---CAGTCAGTCTCTCTTGA 1176
Db 1135 CCTTACCATCAACACAGTGGTCTCTCTTAA 1173
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RESULT 11  
US-10-723-955-13  
; Sequence 13, Application US/10723955  
; Publication No. US20040110238A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lehman-Bruinsma, Karin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Gore, Martin  
; APPLICANT: White, Carol  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors

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; FILE REFERENCE: 7.US29.CON  
; CURRENT APPLICATION NUMBER: US/10/723,955  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 10/417,820  
; PRIOR FILING DATE: 2003-4-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-955-13  
  
Query Match 58.4%; Score 686.6; DB 17; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 2e-209;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
  
Qy 1 ATGTCGGAGTCTAACAGTACTGGGATCTTGGCCACAGCTGCTCAGTCCCTTGGCATTT 60  
Db 1 ATGCAGATATAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
  
Qy 61 TTAATGCTTCAATTTGCTTCTATATGTTAGGCAATGCTGCTGCTATCTTACCTTTT 120  
Db 61 TTTATGTCCTTAGTAGTCTTTTGTCTATAATGTTAGGAAATGCTTTGGTCAATTTAGCTTT 120  
  
Qy 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAAATTTGGCTATTTCT 180  
Db 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAACTTTGCCCATCTCT 180  
  
Qy 181 GACTTCCTCGTGGGTTTGAATTTCCATTCCTCTGTACATCCCTCAGTGTGTTTAACTGG 240  
Db 181 GACTTCTTTGGGTTGATCTCCATTCCTTTGTACATCCCTCAGCGTGTTCGAATGG 240  
  
Qy 241 AATTTTGAAGTGGAAATCTGCATGCTTGGCTCATTACTGACTATCTTTTGTGGCCGCA 300  
Db 241 GATTTTGAAGGAAATCTGTGATTTTGGCTCCTACTGACTATCTGTATGTATGTACAGA 300  
  
Qy 301 TCTGTCTACAATATTTGCTCTCATTAGCTACGATCGATACCAGTCAAGTTTCAAATGCTGTG 360  
Db 301 TCTGTATATACATTTGCTCTCATCAGCTATGATCGATACCTGCTCAGTCTCAAATGCTGTG 360  
  
Qy 361 TCTTATAGGCTCAACACACTGGGATCATGAAGATTTTGTCTCAAATGGTGGCTTTGG 420  
Db 361 TCTTATAGAACTCAACATACATCTGGGTTTGAAGATTTGTACTCTGATGGTGGCTTTGG 420  
  
Qy 421 ATACTGGCTTCTCTGTAATGGCCGATGTTCTGGCTTCAAGTCTTCTTGAAGAACAGC 480  
Db 421 GTGCTGGCTTCTTGTAGTGAATGGGCAATGATTTCTAGTTTCAAGTCTTGGAGGA---- 476  
  
Qy 481 ACGAACAAAGGACTGTGAGCTTGTGTTGTACAGAGTGTATCTCTCACTCACTTACA 540  
Db 477 --TGAAGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534  
  
Qy 541 ATGCTCTTGGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
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Db      535  TCAATCTTGGAAATTCGTGATCCAGTCATCTAGTCGCTTATTTCAACATGAATATTTAT 594
Qy      601  TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGGCCCTACGCCATGCTGGATTCCTCCACT 660
Db      595  TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGGCCCAAGGCCATCTGGACTGACTGCT 654
Qy      661  ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTCTGCAGGACAGTAAT 720
Db      655  GTCTCTTCCAACTCTGTGGACATCTATCAGAGTAGACTATCTTCAAGGAGATCTCTT 714
Qy      721  CCTGGATTGAAGGAATCAGCTGTCATCTGTCCTCAGTACAGAGTCTTCCGAAAGAGAGCAGC 780
Db      715  TCTGCATCGACAGAAGTCTCTGTCATCTTCTCATTTCAGAGACAGAGAGAGAGTAGT 774
Qy      781  ATCTGTGTGCTTAAAGACTCATGAAACAGAGTAGTATCATCTGCTTCAAGAGTGGGTTC 840
Db      775  CTCATGTCTTCCCAAGAACCAAGATGAATAGCAATACAATTGCTTCCAAATGGGTTC 834
Qy      841  TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTAGCAGAGCTTCTCAGAGGC 900
Db      835  TTCTCCCAATCAGATTCCTGATCTCTTCCAAAGGGAGATGTTGAATCTCTTAGAGCC 894
Qy      901  AGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGGCAATTTGCTGGGCTCCA 960
Db      895  AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954
Qy      961  TACTGTCTGTTCACAAATGTCGCTTCAATTCGATGTTCAATTCGTTTAAATCCCTTCTGTAC 1020
Db      955  TATTCCTGTTCACAAATGTCGCTTCAATTCGATGTTTAAATCCCTTCTGTAT 1074
Qy      1021  TGGTACAGCATTCGCTTCTGGCTGCAATGTTCAATTCGTTTGTAAATCCCTTCTGTAT 1080
Db      1015  TGGTATAGAATTCGATTTTGGCTTCAGTGGTTCGATTCGATTCGATTCGATTCGAT 1074
Qy      1081  CCTTGTGTCAAGCGCTTCCAGAGCGCTTCTGGAAGTACTTCTGGAAGTACTTCTGGAAGCAA 1140
Db      1075  CCATTTGTGCACAGCGCTTCCAAAGCGCTTCTTGAAGATATTTTGTATAAAAGCAA 1134
Qy      1141  CCAGCGCTGCACAGAAC---CAGTCAGTATCTTCTTGA 1176
Db      1135  CCTCTACCATCACAAACAGTCGTCGTCAGTATCTTCTTAA 1173

RESULT 12
US-10-737-619-1
; Sequence 1, Application US/10737619
; Publication No. US20040138234A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10737,619
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-737-619-1

Query Match      58.4%; Score 686.6; DB 17; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy      1  ATGTCGAGTCTAACAGTACTGGCATCTTCCACAGCTGCTCAGTCCCTTGGCAATTT 60
Db      1  ATGCCAGATCTAATAGCAATCAATTTATCATAAGCACTCGTGTACTTTAGCAATTT 60
Qy      61  TTAATGTCTTCAATTTGGCTTTGCTTATAATGTTAGGCAATGCTGTGGTCACTTTAGCGCTTT 120

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Db      61  TTAATGTCTTGTAGCTAGCTTTTGGCTATTAATGCTAGAAATGCTTTGGTCAATTTAGCTTTT 120
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Db      121  GTGTGACAGAAACCTTTAGACATCGAAGTAGTTTATTTTCTTAATTTGGCTATTTCT 180
Qy      181  GACTTCTCGTGGGTTTTGATTTCCATTCCCTCTGTACATCCCTCAGCTGTGTGTTAACTGG 240
Db      181  GACTTCTTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCAGCTGTGTGTTAACTGG 240
Qy      241  AATTTTGGAAAGTGAATCTGCATCTTTTGGCTCAATTAAGTCAATCTTTTGTGACCGCA 300
Db      241  GATTTTGGAAAGGAATCTGTGTAATTTTGGCTCACTACTGACTGACTGTAATGTACAGCA 300
Qy      301  TCTGTCTACAAATATTTGCTCATTAGTACGATACGATACCAAGTCAAGTTCAAATTCGTGTG 360
Db      301  TCTGTATATAACATTTGCTCCTCATCAGCTATGATGATACCTGTGCTCAGTCTCAATTCGTGTG 360
Qy      361  TCTTATAGGCTCAACACACTGGCATCATGAGAGATTTGCTCAATTTGGTGGCTTTTGG 420
Db      361  TCTTATAGAACTCAACATACCTGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCGCTTTGG 420
Qy      421  ATACTGGCTTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGGAAAGAACAGC 480
Db      421  GTGCTGGCTTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTTGGAAAGAA--- 476
Qy      481  ACGAACACAAGGACTGTGAGCGCTGCTTTGTTTACAGAGTGGTACATCTCTCACATTACA 540
Db      477  --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTCTTGCCATCACA 534
Qy      541  ATGCTCTTTGGAATTCCTGCTTCTGTCATCTCTGCTGGCTTATTTCAATGTACAGATTTAC 600
Db      535  TCATTTCTTGGAAATTCGTGATCCCGATCATCTTAGTGGCTTATTTTCAACATGAATATTTAT 594
Qy      601  TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGGCCCTAGCCATGCTGGATTTCTCCACT 660
Db      595  TGGAGCCTGTGGAAGCGTAGTATCTCAGTAGGTGGCCAAAGCCATCTGAGTCACTGCT 654
Qy      661  ACCTTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTCGAGGACAAAGTAAT 720
Db      655  GTCTCTTCCAACTCTCTGGACACTATTCAGAGGTAGACTATCTTCAAGAGAGATCTCTT 714
Qy      721  CCTGGATTGAAGNAATCAGCTGCATCTGTCATCTCAGAAAGTCTCTGAAAGAGAGCAGC 780
Db      715  TCTGCATCGACAGAAGTTCCTGTCATCTCTTCAATTCAGAGAGACAGAGAGAGAGTAGT 774
Qy      781  ATCTGTGTCTTAAAGGACTCACATGAACAGAGATATCACTGCTTCAAAAGTGGGTTC 840
Db      775  CTCATGTTTCTTCCAAAGCAAGATGAATAGCAATTAATTTGTTCCAAATGGGTTC 834
Qy      841  TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTAGCAGAGCTTCTCAGAGGC 900
Db      835  TTCTCCCAATCAGATTCCTGATCTCTTCCAAAGGGAGATGTTGAATCTCTTAGAGCC 894
Qy      901  AGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGGCAATTTGCTGGGCTCCA 960
Db      895  AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954
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Db 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCTTAA 1173

RESULT 13

US-10-782-596-13

Sequence 13, Application US/10782596

Publication No. US20040137509A1

GENERAL INFORMATION:

APPLICANT: Chen, Ruoping

APPLICANT: Dang, Huong T.

APPLICANT: Liaw, Chen W.

APPLICANT: Lin, I-Lin

TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

FILE REFERENCE: AREN0050

CURRENT APPLICATION NUMBER: US/10782,596

PRIOR FILING DATE: 2004-02-19

PRIOR APPLICATION NUMBER: US/09/875,076

PRIOR FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: 09/417,044

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,851

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/123,946

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,949

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/136,436

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,437

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,439

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,567

PRIOR FILING DATE: 1999-05-28

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 74

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 1173

TYPE: DNA

ORGANISM: Homo sapiens

US-10-782-596-13

Query Match 58.4%; Score 686.6; DB 17; Length 1173;

Best Local Similarity 75.1%; Pred. No. 28-209;

Mismatches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCCTTTGGCATTT 60

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QY 181 GACTTCTCTGGTGTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTGTTAACTGG 240

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QY 301 TCTGTCTCAATATTTGCTCTCAATCTAGCTAGCATCCAGTCAGCTTTCAATGCTGTG 360

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QY 361 TCTTATAGGCTCAACACACACTGGCATCATGAAGATTTGTCTCAATGGTGGCTGTTGG 420

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QY 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGGNAGAACAGC 480

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RESULT 14

US-09-891-138A-5

Sequence 5, Application US/09891138A

Publication No. US20030083245A1

GENERAL INFORMATION:

APPLICANT: Lin, Daniel Chi-Hong

APPLICANT: Zhao, Jiagang

APPLICANT: Chen, Jin-Long

APPLICANT: Cutler, Gene

APPLICANT: Tularik Inc.

TITLE OF INVENTION: No. US20030083245A1e1 Receptors

FILE REFERENCE: 018781-006210US

CURRENT APPLICATION NUMBER: US/09/891,138A

CURRENT FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: US 60/213,461

PRIOR FILING DATE: 2000-06-23

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; SOFTWARE: PatentIn Ver. 2.1
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)...(1197)
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-5

Query Match      58.4%; Score 686.6; DB 10; Length 1266;
Best Local Similarity 75.1%; Pred. No. 2.1e-209;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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Db 1 ATGTCGGAGTCTAACAGTACTGGCACTTGGCCAGCTGTCAGGTCCCTTGGCATT 60
QY 25 ATGCCAGATACCTAATAGCACAACTCAATTTATCACTAAGCACTCGTGTACTTTAGCAAT 84
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Db 181 GACTTCCTCGGGTTTGAATTTCCATCTCTGTACATCCCTCAGGTGTTGTTAACTGG 240
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Db 205 GACTTCCTTGGGGTGTGATCTCCATCTCTTGTACATCCCTCAGGTGTTGTTAACTGG 264
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Qy 481 ACGAACACAAAGGACTGTGAGCTGGCTTTGTACAGAGTGATACATCTCAACATTACA 540  
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Db 635 TGGAGCCTGTGAAGGGTGATCATCTCAGTAGTGGCCAAAGCCATCTTGGACTGCTGCT 694  
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Job time : 667 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	129.2	11.0	853	14	CD326085
6	115.6	9.8	684	29	CC481311
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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 839)  
Fober, G., Han, M. and Wiemann, S.  
EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)  
Unpublished (2003)  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp781C0629) is available at the RZPD in Berlin.

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AY400784 Mus muscu  
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CD804122 UI-M-GV0-  
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BE783826 601471053  
BU107479 BU107479

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers  
1. 839

## FEATURES

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cDNA collection"

## ORIGIN

Query Match 37.3%; Score 438.6; DB 13; Length 839;  
Best Local Similarity 75.9%; Pred. No. 7.7e-100;  
Matches 570; Conservative 0; Mismatches 174; Indels 7; Gaps 2;

QY 1 ATGTCGGAGCTAACAGTACTGGCATCTTGGCACCAGCTGCTCAGGTCCCTTGGCATTT 60  
DB 96 ATGCCAGATACCTAATAGCACATCAATTTATCCTAGCAGCTCGTGTACTTTAGCATTT 155  
QY 61 TTAATGTTCTTCAATTTGGCTTGTCTATAATGTTAGGCAATGCTGTGGTCACTTTAGCCCTTT 120  
DB 156 TTATGTCCTTAGTACCTTTTGTATATGCTAGGAATGCTTTGGTCACTTTAGCTTTT 215  
QY 121 GTGTGGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTCT 180  
DB 216 GTGTGGGACAAACCTTAGACATCGAAGTAGTATTTTTTCTTAACCTTGGCCATCTCT 275  
QY 181 GACTTCTCTGGTGGTTGATTTCCATCTCTGTACATCCCTCAGCTGTGTTAACTGG 240  
DB 276 GACTTCTTGTGGGTGATCTCCATCTCTTTGTACATCCCTCAGCTGTGTTAACTGG 335  
QY 241 AATTTTGGAAAGTGGAAATCTGATGTTTGGCTCAATCTACTGACTATCTTTTGTGCAACGCA 300  
DB 336 GATTTTGGAAAGAAATCTGTGATTTTGGCTCAGTACTGACTATCTGTTATGTACAGCA 395  
QY 301 TCTGTCTACAATATTGTCCTCAATAGTACGATCGATGAGTACGATGCTTTCAATGCTGTG 360  
DB 396 TCTGTATATAACATTTGCTCTCATCATGATGATGATGATGATGATGATGATGATGATGATG 455  
QY 361 TCTTATAGGCTTCACACACTCGCATCATGAGATTTGCTCAATGTTGGTGGCTGTTGG 420  
DB 456 TCTTATAGAACTCAACATCTGCGGTCTTGAAGATTGTTACTCTGATGTTGGCGTTGG 515  
QY 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTTGGAAAGACAGC 480  
DB 516 GTCTGGCTTCTTAGTGAATGGCCAAATGATTTCTAGTTTCAGAGTCTTGGAAAGGA- 571  
QY 481 AGAACACAAAGACCTGTGAGCGCTGCTTTGTACAGAGTGGTACATCTCCACATTACA 540  
DB 572 --TGAAGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTGGCATCACA 629  
QY 541 ATGCTCTTGGAAATTCCTGCTTCTCTGTCATCTGCTGCTTATTTCAATGTACAGATTTC 600  
DB 630 TCAATCTTGAATTCGTGATPCCAGATCATCTTAGTGCCTTATTTCAACATGAATTTAT 689  
QY 601 TGGAGCTGTGGAAGCGTAGGGCTCTCAGTAGTGCCCTAGCCATGCTGGATTTCTCCACT 660  
DB 690 TGGAGCTGTGGAAGCGTGTATCATCTCAGTAGTGCCAAAGCCATCTCGACTGACTGCT 749  
QY 661 ACCTTTCCAGTCTTCAGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720  
DB 750 GTCTCTTCCACATC-TGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 808  
QY 721 CCTGGATTGAAGGAATCAGCTGATCTCGTC 751  
DB 809 TCTGCAATCGAAGATTCTGCAATCTTTC 839

RESULT 2

CFI147821

LOCUS

DEFINITION

AGENCOURT 14740195 NIH MGC 145 Homo sapiens cDNA clone

IMAGE:6971900 5', mRNA sequence.

ACCESSION

CFI147821

VERSION

CFI147821.1 GI:33244089

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (Bases 1 to 704)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: GPCR Consortium

cDNA Library Preparation: GPCR Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Cloning Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRBI02 row: b column: 07

High quality sequence stop: 685.

Location/Qualifiers

1..704

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6971900"

/tissue\_type="mixed"

/lab\_host="DH10B"

/clone\_lib="NIH MGC 145"

/note="Vector: pcDNA3.1; Site\_1: varies by clone; Site\_2:

varies by clone; ORFs were PCR-amplified and cloned into

pcDNA3.1 by the GPCR Consortium. Cloning sites vary by

clone and include the following: 5'-EcoRV-XmaI/XhoI-3',

5'-EcoRV-XmaI/NotI-3', EcoRV (TA cloned, non-directional).

For information about which gene each clones represents,

please visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed\_plates/IRBI.presv.dat

a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match

Best Local Similarity

Matches 547; Conservative

36.3%; Score 426.4; DB 14; Length 704;

77.0%; Pred. No. 9e-97;

Mismatches 156; Indels 7; Gaps 2;

QY 3 GTCCGAGTCTAACAGTACTGGCATCTTGGCACCAGCTGCTCAGGTCCCTTGGCATTTT 62

DB 1 GCCAGATACATAGACAAATCAATTTATCATAGCACTCGTGTACTTTAGCATTTT 60

QY 63 AATGCTCTCATTTGCTTGTCTATAATGCTAGGCAATGCTGTGCTCATCTTAGCCTTTGT 122

DB 61 TATGCTCTTAGTACCTTTTGTCTATAATGCTAGGAATGCTTTGCTCATTTAGCTTTGT 120

QY 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTTCTTAATTTGGCTATTCTGA 182

DB 121 GGTGGACAAACCTTAGACATCGAAGTAGTATTTTTTTCTTAACCTGGCCATCTGA 180

QY 183 CTTTCCTCGTGGTTCGATTCCTTCCATCTCTGTACATCCCTCAGCTGTGTTTAACCTGGA 242

DB 181 CTTTCCTCGTGGTTCGATTCCTTCCATCTCTTGTACATCCCTCAGCTGTGTTGAATGGA 240

QY 243 TTTTGAAGTGGAAATCTGATGTTTGGCTCATTACTGACTATCTTTTGTGACCGCATC 302

DB 241 TTTTGAAGAAATCTGATGTTTGGCTCATTACTGACTATCTGTTATGTATGATGACGATC 300

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QY 303 TGTCTACAATATTGCTCTCATTTAGCTACGATCGATACAGCTCAGTTTCAAAATGCTGTGTC 362
Db 301 TGTATATAACATTGCTCTCATCAGCTATGATCGATACGATCGATCTCAATATGCTGTGTC 360
QY 363 TTATAGGCTCAACACACAGCTGGCATCATGAAGATTGTTGCTCAATGGTGGCTGTTTGGAT 422
Db 361 TTATAGAACTCAACATACTGGGGCTTGAAGATTGTTTACTCTGATGGTGGCGGTTTGGGT 420
QY 423 ACTGGCTTTCTTGTGTAATGGCCCATGATTTCTGGCTTCAGATTTCTGGAAGACAGCAC 482
Db 421 GCTGGCTTCTTAGTGAATGGCCAAATGATTTCTAGTTTCAAGATCTTGGAGGA----- 474
QY 483 GAACACAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCACCATTACAAAT 542
Db 475 TGAAGTAGTGAATGTAACCTGGATTTTTTGGGAATGGTACATCTTGGCAATCACATC 534
QY 543 GCTCTTGAATTCCTGCTCTGCTGTCATCTCTGTGCTTATTTCAATGTACAGATTACTG 602
Db 535 ATTCTTGGAAATTCGTGATCCAGTCATCTTAGTCTGCTTATTTCAACATGAATATTTATTG 594
QY 603 GAGCCTGTGGAAGCTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTTCCACTAC 662
Db 595 GAGCCTGTGGAAGCTGATCATCTCAGTAGGTGCCAAGCCATCTCGACTGACTGCTGT 654
QY 663 CTCTTCAGTCTTCAGACACTTACACAGAGCTGGGGTGGCTTGCAGGA 712
Db 655 CTCTTCCACATC-TGTGGACACTCATTCAGAGGTAGACTATCTTTTCAGGA 703

RESULT 3
CB556920
LOCUS
DEFINITION
  AMGNNUC:URGP1-00001-d6-A urgp1 (14349) Rattus norvegicus cDNA clone
  urgp1-00001-d6 5', mRNA sequence.
ACCESSION
  CB556920
VERSION
  CB556920.1 GI:29496320
KEYWORDS
  EST.
SOURCE
  Rattus norvegicus (Norway rat)
ORGANISM
  Rattus norvegicus
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  Rattus.
REFERENCE
  1 (bases 1 to 672)
  Angen EST Program.
  Angen Rat EST Program
  Unpublished (2003)
  Contact: Dan Fitzpatrick
  Angen, Inc
  One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
  Tel: 805 447-4881
  Plate: 00001 row: d column: 6.
  Location/Qualifiers
    1..672
    /organism="Rattus norvegicus"
    /mol_type="mRNA"
    /db_xref="taxon:10116"
    /clone="urgp1-00001-d6"
    /clone_lib="urgp1 (14349)"
    /note="Vector: pSPORT1; Rat GPCR library rearrayed
    internal pSPORT vector"

ORIGIN
Query Match 11.5%; Score 135.8; DB 14; Length 672;
Best Local Similarity 57.2%; Pred. No. 2.2e-23;
Matches 267; Conservative 0; Mismatches 197; Indels 3; Gaps 1;

QY 3 GTCCGAGTCTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCAATTTT 62
Db 178 GGCCTGTGACGGCGGGCGCGGCTTCTCGGCTGCTGACCGCTCTCTGCTGGCT 237
QY 63 AATGCTCTTCAATTGCTCTATATAGTAGGCAATGCTGTGGTCACTTACGCTTTGT 122
Db 238 CATGGCGTCTCATCTGTGGCCACAGTACTGGGCAACGGCTGGTATGCTCGCTTGT 297

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QY 123 GGTGACAGAAACCTTAGACATTCGAGTAATATTTTTTCTTAATTTGGCTATTTCGA 182
Db 298 GCGGATTCGAGCCTCCGACACCCAGAACAACTTCTTTCTGTCTCAACCTCGCATCTCCA 357
QY 183 CTTCCTCTGGTGTGATTTCATTTCCATTCCTCTGACATCCCTCAGCGTGTGTTAAC---TG 239
Db 358 CTTCCTCTGGTGTGCTTCTGATCCCAATTTGATACCCCTATGTGCTGACCGGCGGTG 417
QY 240 GAATTTTGGAGTGGAAATCTGCATGTTTGTGCTCATTTACTGACTATCTTTTGTGCACGCG 299
Db 418 GACCTTCGGCGCGGCTCTTCAAGCTGTGGCTGTGCTGAGTACTTACTTGTGTGCTC 477
QY 300 ATCTGCTTACAAATATTGCTTCTATAGCTAGTACATGATACAGTACAGTTTCAATGCTGT 359
Db 478 CTCGGTCTTCAACATCGTACTCATCAGCTATGACCGATTCCTGTGCTGAGTCACTCGAGCTGT 537
QY 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTGCTGCTCAAAATGGTGGCTGTTTG 419
Db 538 CTCCTACAGGCCACAGAGGGGACAGAGCGGCGCTTCGGAAGATGGCACTGGTGTG 597
QY 420 GATACTGGCTTCTTGTGTAATGGCCGATGATTCTGGCTTTCAGATT 466
Db 598 GGTGCTGGCCTTCTCTGTGATGGCTGCCATCTCGATTTGGGAGT 644

RESULT 4
CF147822
LOCUS
DEFINITION
  AGENCOURT 14740187 NIH MGC 145 Homo sapiens cDNA clone
  IMAGE:6971899 5', mRNA sequence.
ACCESSION
  CF147822
VERSION
  CF147822.1 GI:33244090
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 732)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Daniela S. Gerhard, Ph.D.
  Office of Cancer Genomics
  National Cancer Institute / NIH
  Bldg. 31 Rm10A07 Bethesda, MD 20892
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: GPCR Consortium
  cDNA Library Preparation: GPCR Consortium
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: IRB102 row: b column: 06
  High quality sequence stop: 610.
  Location/Qualifiers
    1..732
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:6971899"
    /tissue_type="mixed"
    /lab_host="DH10B"
    /clone_lib="NIH MGC 145"
    /note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
    varies by clone; ORFs were PCR-amplified and cloned into
    pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
    clone and include the following: 5'-EcoRV-XmaI/XhoI-3',
    5'-EcoRV-XmaI/NotI-3', EcoRV (TA cloned, non-directional).
    For information about which gene each clone represents,
    please visit our anonymous ftp site at
    http://image.llnl.gov/image/rearrayed\_plates/IRB1.preSV.dat

```

FEATURES  
source

a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 11.4%; Score 133.8; DB 14; Length 732;  
Best Local Similarity 53.5%; Pred. No. 7.3e-23;  
Matches 329; Conservative 0; Mismatches 277; Indels 9; Gaps 2;  
QY 3 GTCGAGTCTAACAGTACTGTCATCTCCACAGCTGCTCAGTCCCTTGGCATTTT 62  
DB 76 GCGCGCGCGCGCGCGCGCTTCTCGCAGCTGCGCGGCTGCGCGCGCT 135  
QY 63 AATGCTTTCATTTGCTTTGCTATATGCTAGGCAATGCTGGTCACTTTAGCTTTGT 122  
DB 136 CATGCGCTGCTCATCTGTTGCGACGCTGCTGGCAACGCTGCTGCTGCTGCTTGT 195  
QY 123 GGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTTTCTTAATTTGGTATTCTGA 182  
DB 196 GCGGACTCGAGCTCCGACCCAGCAACACTTCTCTGCTCAACCTCGCCATCTCGA 255  
QY 183 CTTCCTGCTGGTTGATTTCATTCCTCTGTACATCCCTCACGCTGTG---TTTAATG 239  
DB 256 CTTCCTGCTGGCGCTTCTGCACTCCACTGTATGACCTACCTGCTGCTGCTGCTG 315  
QY 240 GAATTTTGAAGTGAATCTGATGTTTGGCTCACTACTGACTATCTTTTGTGACCGC 299  
DB 316 GACCTTCGCGCGCGGCTCTGCAAGCTGGCTGGTGTAGTGAATCTGCTGCACTC 375  
QY 300 ATCTGCTACAAATTTGCTCCTCATTTAGTACGATACATACAGTCAAGTTTCAATGCTGT 359  
DB 376 CTCCTGCTTCAACATCGTCTCATCAGCTACGACGCTTCTCTGCTGCTGCTGCTGCT 435  
QY 360 GTCTTATAGGCTCAACACATCGGCTCATGAAGATTGTTGCTCAATGGTGGCTGTTG 419  
DB 436 CTCATACGCGGCGGCGGCTGACACGCGGCGGCGAGTGGCGAAGATGCTGCTGTTG 495  
QY 420 GATCTGCTTCTTCTGTAATGCGCGGCTGATCTGCTGCTTCTGCTTCTGCTTCTG 473  
DB 496 GGTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555  
QY 474 GAACAGCAGCAACACAAAGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533  
DB 556 CAGCTCCATCCCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615  
QY 534 CATTACAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593  
DB 616 CAGGCTTCCACACTGAGTCTTCTAGCGGCTTCTAGCGGCTTCTAGCGGCTTCT 675  
QY 594 GATTACTGGAGCT 608  
DB 676 CATCTACCTGAACAT 690

RESULT 5

CD326085 853 bp mRNA linear EST 28-MAY-2003  
LOCUS AGENCOURT 14163426 NICHG\_XGC\_Eye1 Xenopus laevis cDNA clone  
DEFINITION IMAGE:6949081 5', mRNA sequence.

ACCESSION

CD326085  
CD326085.1 GI:31090416  
EST.  
Xenopus laevis (African clawed frog)

KEYWORDS

Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus.  
1 (bases 1 to 853)

REFERENCE

NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement:

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM14564 row: f column: 24

High quality sequence stop: 707.

FEATURES

source

1..853  
Location/Qualifiers  
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/mol\_type="mRNA"  
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/clone="IMAGE:6949081"  
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/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NICHG\_XGC\_Eye1"  
/note="Organ: eye; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dr.  
Average insert size 2.3 kb. Constructed by Life  
Technologies. Note: This is a Xenopus Gene Collection  
(XGC) library."

ORIGIN

Query Match 11.0%; Score 129.2; DB 14; Length 853;  
Best Local Similarity 58.7%; Pred. No. 1.1e-21;  
Matches 243; Conservative 0; Mismatches 168; Indels 3; Gaps 1;  
QY 45 GGTCCCTTGGCAATTTAAATGCTTCAATTTGCCCTTGTCTAATAATGGTAGGCAATGCTGT 104  
DB 381 GGTCTTCTCGGCTGCTCTGATGGGGTCTCTCATAGTTAGCACCGTGTGGGAATGCCCT 440  
QY 105 GGTCTCTTAGCTTGTGCTGGCAGACAACTTAGACATCGAAGTAATTTATTTTCT 164  
DB 441 GGTCTAGTGGCTTTTGTGTTGGACTCCAGCTCCGACCCAGAAATTAATTTCTCTTCT 500  
QY 165 TAATTTGGCTATTCTGACTTCTCTGTTGGTTTGAATTTCCATTTCTCTGTACATCCCTCA 224  
DB 501 CAACCTGGCTATCTCAGATTCTTTGTAGTCCCTGTGCATCCCTCTCTATGTGCCATA 560  
QY 225 CGTGTGTTT---AACTGGAATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTAATGTA 281  
DB 561 CGTACTGACTGCGAGATGAGCTTTGGCAGAGCGCTTTGCAAACTGTGGCTGGTCTGGA 620  
QY 282 CTATCTTTTGTCCACCGCATCTCTACAATATTTGCTCTATTAGCTACGATCGATACCA 341  
DB 621 TTATCTGCTCTGCACCTCGTCCGTGTTCAACATCGTGTCTCATCAGCTACGACAGTT 680  
QY 342 GTCAGTTTCAAAATGCTGTCTTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTC 401  
DB 681 CTCTGTGACCCGGCTGTCTAGTTACCGAGCTCAGCAGAGTAACAGCCGGCATCGACTTT 740  
QY 402 TCAAAATGGTGTGTTTGGATGACTGCTTTCTTGTAAATGGCCCATGATTTCT 455  
DB 741 GAAATGACCATGGTGTGGATCTTTGGCTTTCTCTATATATGGACCAATTAAT 794

RESULT 6

CC481311

LOCUS

DEFINITION

CC481311

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 684)

CC481311 684 bp DNA linear GSS 16-JUN-2003  
CH240\_309C10.T7 CHORI-240 Bos taurus genomic clone CH240\_309C10,  
genomic survey sequence.



## AUTHORS

Holt, R., Stott, J., Yang, G., Barber, S., Smalhus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B. P., and Tellam, R.  
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398  
Unpublished (2003)  
Other GSSs: CH240\_309C10.TARBAC13P2  
Contact: Rob Holt

## TITLE

## JOURNAL

## COMMENT

Sequencing  
The British Columbia Cancer Agency Genome Science Centre  
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6  
Tel: 604-877-6085  
Fax: 604-877-6276  
Email: rholt@bcgsc.ca

Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong ([pdejong@mail.choi.org](mailto:pdejong@mail.choi.org)). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/ordering/information.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.

Plate: 309 row: C column: 10

Seq primer: T7

Class: BAC ends.

## FEATURES

source

Location/Qualifiers

1..684

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="breed: Hereford"

/db\_xref="taxon:9913"

/clone="CH240\_309C10"

/sex="Male"

/cell\_type="Blood"

/clone\_lib="CHORI-240"

/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Dominio 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 9.8%; Score 115.6; DB 29; Length 684;  
Best Local Similarity 70.6%; Pred. No. 2.8e-18;  
Matches 154; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 150 TAATATATTTTCTTAATTTGGCTATTTCTGACTTCCTCGTGGGTTTGATTTCCATTC 209  
DB 260 TAGGTGCTATATTTGTTAATCTTCAATTTTTCGCCCATGCGAGTATGATCTCCATTC 319

QY 210 TCTGTACATCCCTCACGCTGTTGTTAACTCGAATTTTGGAGTGGATCTGCATGTTTG 269  
DB 320 TTATTCATCCCTCACAGCTCTTCAACTGGAGTTTGAATAAACAATTTGTGCTTTTG 379

QY 270 GCTCATTAAGTACTATTTTGTGACCGCATCTGTCTACAATATTTGCTCTCATTAAGCTA 329  
DB 380 GCTCACTACTGACTATCTTTTGTGACAGCATCTGTGTATTAACATGCTACTCATGCTT 439

QY 330 CGATCATACAGTCTAGTTTCAATGCTGTGCTTATA 367  
DB 440 TGATCATATCATGTCAGTCTCCAATGCTGTAAGTCAAA 477

## RESULT 7

AL848045

LOCUS

DEFINITION AL848045 XGC-egg Silurana tropicalis cDNA clone Tegg022122 5', mRNA sequence.

ACCESSION AL848045

VERSION

KEYWORDS

SOURCE

ORGANISM

643 bp mRNA linear EST 26-NOV-2003

643 bp mRNA linear EST 26-NOV-2003

643 bp mRNA linear EST 26-NOV-2003

643 bp mRNA linear EST 26-NOV-2003

643 bp mRNA linear EST 26-NOV-2003

643 bp mRNA linear EST 26-NOV-2003

643 bp mRNA linear EST 26-NOV-2003

643 bp mRNA linear EST 26-NOV-2003

643 bp mRNA linear EST 26-NOV-2003

643 bp mRNA linear EST 26-NOV-2003

643 bp mRNA linear EST 26-NOV-2003

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Silurana.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

1 (bases 1 to 643)  
Sanger Xenopus tropicalis EST project 2001 (11\_2003)  
Unpublished (2003)

On Sep 15, 2002 this sequence version replaced gi:22868310.

Contact: Taylor R

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: [tr@sanger.ac.uk](mailto:tr@sanger.ac.uk)

Sanger Xenopus tropicalis EST project 2001

TROPICALIS\_SEQUENCE\_ID: Tegg022122.plkSP6

Sequencing primer: SP6

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

cDNA was oligo dT primed from Sug of poly A+ RNA from egg.

ECORI-NotI cut cDNA was then ligated into pCS107 with EORI at the

5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EORI; Site 2: NotI

Host: Escherichia coli XL1-blue.

## FEATURES

source

1..643

/organism="Silurana tropicalis"

/mol\_type="mRNA"

/db\_xref="taxon:9364"

/clone="Tegg022122"

/dev\_stage="egg"

/lab\_host="Escherichia coli XL1-blue"

/clone\_lib="XGC-egg"

/note="Vector: pCS107; Site 1: EORI; Site 2: NotI; cDNA

was oligo dT primed from Sug of poly A+ RNA from egg.

ECORI-NotI cut cDNA was then ligated into pCS107 with

ECORI at the 5' end and NotI at the 3' end"

## ORIGIN

Query Match 8.4%; Score 99; DB 9; Length 643;  
Best Local Similarity 55.5%; Pred. No. 4.4e-14;  
Matches 236; Conservative 0; Mismatches 180; Indels 9; Gaps 2;

QY 193 GGTGTTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTT---AACTGGAATTTGGA 249  
DB 83 GTGGGATTCGTATCCCACTCTATATCCCTTATGTGCTGACTGCGCCAGTGGAGTTGGG 142

QY 250 AGTGGAAATCGCATGTTTGGCTCATCTACTGACTATCTTTTGTGCGACCGCATCTGCTAC 309  
DB 143 AAAGGCTTGTGCAAGTTGTGCTAGTAGTAATGAGTACTACCTTTTATGCACTGCTTCAGTTT 202

QY 310 AATATTGCTCTATTAGTACGATCGAATCCAGTCCAGTTCAGTTTCAAATGCTGTGCTTATAGG 369  
DB 203 AATATTGCTCTATCATGATGATGACAGTTTCATCTCAGTCACTAAAGCGGTGCTCTACAGA 262

QY 370 GCTCAACACACTGGCATCATGAAGATGTTGCTCAATGGTGGCTGTTTGGTACTGCTGCT 429  
DB 263 GCACAGAAAGGAATGACAGAAATGCAAGTGTAAATGCTTATTTGTTGGTGGCAGCC 322

QY 430 TTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGA-----TTCTTGGAAAGAACAGCAGC 483  
DB 323 TTCTTCTCTATGCGCCAGCCATCATCACCTGGGAATACATTCGAGAACTACTATCTTA 382

QY 484 AACACAAAGGACTGTGAGCGCTGCTTTGTTACAGAGTGGTACATCCCTCAATTAACAATG 543  
DB 383 CCAGAAAGGGGAATGTTATGTAGAATTTCTACTCAACTGGTATTTTCTGATGATAGCTTCC 442

QY 544 CTCTTGGAAATTCCTGCTCTCTGTCATCTCTGCGCTTATTTCAATGACAGATTTACTGG 603  
DB 443 ACATAGAAATCTTTTACTCAATTCATCAGTGTTCCTTATTTCAATCTAAGCATCTACAT 502

QY 604 AGCCT 608  
DB 503 AACAT 507

RESULT 8  
 BF567596  
 LOCUS  
 DEFINITION  
 UI-R-B00-agr-c-06-0-UI.r1 UI-R-B00 Rattus norvegicus cDNA clone  
 UI-R-B00-agr-c-06-0-UI 5', mRNA sequence.  
 ACCESSION  
 BF567596  
 VERSION  
 BF567596.1 GI:11677326  
 KEYWORDS  
 EST.  
 SOURCE  
 Rattus norvegicus (Norway rat)  
 ORGANISM  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 499)  
 REFERENCE  
 AUTHORS  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL  
 Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE  
 97044477  
 PUBMED  
 8889548  
 COMMENT  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEHRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
 clones will be available through Research Genetics (www.resgen.com)  
 This clone is also available through the I.M.A.G.E. Consortium at  
 LLNL (info@image.llnl.gov). IMAGE ID= 1796445  
 Seq primer: M13 Forward

## FEATURES

source  
 1..499  
 Location/Qualifiers  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-B00-agr-c-06-0-UI"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="UI-R-B00"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The library  
 (UI-R-B00) is a subtracted library derived from a mixture  
 of the following tissues: thalamus, cerebellum,  
 hypothalamus, medulla, pons, midbrain, cerebral  
 corpus striatum and hippocampus. For a detailed  
 description of the library from which this clone was  
 derived, please visit our web site at  
 ratseq.eng.uiowa.edu. The subtraction has been previously  
 described in (Bonaldo, Lennon and Soares, Genome Research  
 6:791-806, 1996)"

## ORIGIN

Query Match 8.1%; Score 95.6; DB 10; Length 499;  
 Best Local Similarity 54.5%; Pred. No. 3e-13;  
 Matches 238; Conservative 0; Mismatches 190; Indels 9; Gaps 2;  
 QY 192 GGGTTTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTTAAAC---TGGAAATTTGG 248  
 Db 58 GGGTGCCCTTCGATCCCATTCAGTACCTATGTGCTACCGCGCGTGGACCTTCGG 117  
 QY 249 AAGTGAATCGCATGTTTGGCTCATTACTGACTATCTTTTGTGACCGCATCTGCTA 308  
 Db 118 CCGGGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACCTACTGTGTGCCCTCGGTCCT 177  
 QY 309 CAATATTGTCCTCATTAGTACGATGATACCATCAGTTCAGTTTCAAATCCTGTGCTTATAG 368  
 Db 178 CAACATCGTACTCATAGCTATGACCAATTCCTGTAGTCACTCGACTGTCTCCACAG 237  
 QY 369 GGCTCAACACATGGCATCATGAAGATTGTTGCTCAAAATGGTGCTGTTGGATCTGGC 428

Db 238 GGGCCAGCAGGGGGACACGAGACGGCGCGTTGGGAAGATGGCACTGGTGTGGGTGCTGGC 297  
 QY 429 TTCTTTGTAATAATGSCCGGATGATTCTGGCTTCAGA-----TTCTTGAAGAACAGCAC 482  
 Db 298 CTTCCTGCTGTATGGGCGCTGCATCTCCTAGTTGGAGTACCTGTCTGGTGGCAGTTCCAT 357  
 QY 483 GAACACAAAGGACTGTGAGCCCTGGCTTTGTACAGAGTGGTACATCCTCCACCATTAACAT 542  
 Db 358 CCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAACTGGTACTTCTCATCAGGNCCTC 417  
 QY 543 GCTCTTGAATTCCTGCTTCTGCTCATCTCTGTGCTTATTTCAATGACAGATTACTG 602  
 Db 418 CACCCTCGAGTTCTTACGCGCCTTCTCAGCGTTACCTTCTTCAACCTCAGCATCTACCT 477  
 QY 603 GAGCCTGTGGAGCGTA 619  
 Db 478 GAACATCCAGAGCGCA 494

## RESULT 9

BQ950659  
 LOCUS  
 DEFINITION  
 AGENCOURT\_8863943 NIH\_MGC\_129 Mus musculus cDNA clone IMAGE:6311932  
 5', mRNA sequence.  
 ACCESSION  
 BQ950659  
 VERSION  
 BQ950659.1 GI:22366137  
 KEYWORDS  
 EST.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 1046)  
 REFERENCE  
 AUTHORS  
 NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL  
 Unpublished (1999)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: Susan L. Sullivan, PhD.  
 cDNA Library Preparation: ResGen, Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM13736 row: k column: 05  
 High quality sequence stop: 640.

## FEATURES

source  
 1..1046  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6311932"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_129"  
 /note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;  
 Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.  
 Primer: Oligo dt. Average insert size 2.2 kb. Constructed  
 by ResGen, Invitrogen Corp. Note: this is a NIH\_MGC  
 Library."

## ORIGIN

Query Match 7.5%; Score 88.6; DB 13; Length 1046;  
 Best Local Similarity 61.6%; Pred. No. 2e-11;  
 Matches 141; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 QY 238 TGAATTTGGAAGTGAATCTGATGTTTGGCTCATTAATCACTATCTTTGTGCACC 297  
 Db 488 TGAACCTTTGGCGGGCCCTCTCAAGCTGTGGTGGTAGACTACCTACTGTGTGCC 547  
 QY 298 GCATCTGTCTACAAATATTGTCCTCAATTAGCTACGATCAGTACCAGTTCAGTTTCAAATGCT 357  
 Db 548 TCCTCAGTCTTCAACATCGTGTGCTGATCAGCTATGACCGATTCTCTGTGAGTCACTCGAGCT 607

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QY 358 GTGCTTATAGGCTCAACACACTGGCATCAATGAAGATTGTTCTCAAAATGGTGCTGTT 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 608 GTCTCTACCGGGCCAGCAGGGGACACAGACGGGCTGTTCGGAAGATGGCACTGGTG 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 TGGATACCTGGCTTTCTTGGTAAATGGCCGATGATTCCTGGCTTCAGATT 466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 668 TGGGTGCTGGGCTTCTCTGTATGGGCTGGCATCTGAGTTGGGAGT 716
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
LOCUS CN503296/c
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
206D09 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL224547
VERSION AL224547.1 GI:7883412
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizanes,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 921)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
source
Location/Qualifiers
1. .921
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="206D09"
/clone_lib="G"
/note="Genoscope sequence ID : COAG206C805LP1-end : T7"

ORIGIN
Query Match 7.4%; Score 87.6; DB 29; Length 921;
Best Local Similarity 59.0%; Pred. No. 3.5e-11;
Matches 170; Conservative 0; Mismatches 114; Indels 4; Gaps 1;

QY 889 CTTCTCAGAGGCAGGAGTCAGCAGGTCACTGGCCATCTTCGAGCGCTTTGCCATT 948
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 588 CTGTCCAGACAAAGATTGCCAATCTCTGCCCATATCGTCTGTATTTTCGGGATC 529
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 949 TGTGGGCTCCATCTGCTGTTCACAAATGTCTCTTCAACTACCCGAGAACGACGC 1008
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 528 TGCTGGGCCCTCACACGCTGCTGATGATCATCCGGCGCTGCAGCGCAGGTGGTGG 469
QY 1009 CCCAAATCGGTGGTGGTACAGCATGCTTCTGGCTGCAATGGTTCAAATCGTTTGTAA 1068
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 468 CCGACTAC-----TGGTACGAGATAACCTTCTGGCTCCTGTGGCTCAACTCAGCCATCAAC 413
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1069 CCCTTCTGTATCCCTTGTGTCAGGGGTTTCCAGAGGGTTTCTCGAAGGATCTTGT 1128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 412 CCCTTCTGTATCCCGCTGTGCCAGAGCTTCCGAGGGCTTCTCCAGATCCTGCTGT 353
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1129 GTGCAAGCAACCGCGCTGTCTACAGAACCGTCAAGTCAAGTATCTTCTTGA 1176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 352 CCCAAAGACAGTCCGTTCAGCTCAGATCGAAGTCCAGTCTGTGTAA 305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
LOCUS BU468854
DEFINITION 603373878F1 CSEQRBN20 Gallus gallus CDNA clone CHEST284119 5', mRNA
sequence.
ACCESSION BU468854
VERSION BU468854.1 GI:25962431
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 754)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES
source
Location/Qualifiers
1. .754
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST284119"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate
cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRBN20"
/note="Vector: pBluescript II KS(+); Site 1: EcoRI;
Site 2: NotI; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunted, ligated to
NotI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldo et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."

ORIGIN
Query Match 6.9%; Score 80.6; DB 13; Length 754;

```



/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."

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ORIGIN
Query Match      6.8%; Score 80.2; DB 10; Length 258;
Best Local Similarity 59.1%; Pred. No. 2.1e-09;
Matches 136; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 237 CTGGAATTTTGAAGTGAATCGCATGTTTGGCTCATCTAGTACTATCTTTTGTGCAC 296
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
4 CTGGCCCTTCGCCGGGGCTCTGAAGCTGTGGTGTGGCGGACTACCTCTCTGCCC 63

QY 237 CGCATCTGTCTACATAATTTGCTCTATTAGCTACGATCGATACCACTAGTTCATCAATGC 356
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
64 CTCCTCTGTCTCATATCGCGCTCATCAGCTATGACCGCTTCCTGTGGNACCCGAGC 123

QY 357 TGTGTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTGTCAAAATGGTGGCTGT 416
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
124 CGTCTCTTACCGGACCCAGCGGTGACACGGCGCGGCGAAGACAGATGGTCTGGT 183

QY 417 TTGATACTGGCTTCTTGGTAAATGGCCCGCATGATTCTGGCTTCAGATT 466
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
184 GTGGTGTGGCTTCTCTCTATGGACCCCGCATCTCTAGTTGGGAGT 233

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RESULT 14
B0836551
LOCUS      410 bp      mRNA      linear      EST 09-JAN-2003
DEFINITION rfa7c11.y1 Meloidogyne hapla J2 pAMP1 v1 Meloidogyne hapla cDNA 5',
similar to TR:Q9XW31 Q9XW31 Y40H4A.1 PROTEIN. [1] ;, mRNA sequence.
ACCESSION  B0836551
VERSION    B0836551.1 GI:22140865
KEYWORDS
SOURCE
ORGANISM  Meloidogyne hapla
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heterodidae; Meloidogyninae; Meloidogyne.
1 (bases 1 to 410)
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Tsagarishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schuck,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone will not be made available due to an unidentified
microbial contamination of the source material.
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. .410
/organism="Meloidogyne hapla"
/mol_type="mRNA"
/db_xref="taxon:6305"
/dev_stage="J2"
/lab_host="DH10B"
/clone_lib="Meloidogyne hapla J2 pAMP1 v1"
/note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The cDNA was
made by using Dynabead oligo-dT priming (Dynal). PCR based
library using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of pAMP1. J2 were provided by Dr. Valerie

```

```

FEATURES
source
1. .410
/organism="Meloidogyne hapla"
/mol_type="mRNA"
/db_xref="taxon:6305"
/dev_stage="J2"
/lab_host="DH10B"
/clone_lib="Meloidogyne hapla J2 pAMP1 v1"
/note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The cDNA was
made by using Dynabead oligo-dT priming (Dynal). PCR based
library using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of pAMP1. J2 were provided by Dr. Valerie

```

Williamson of the University of California at Davis  
(vmwilliamson@ucdavis.edu)."

```

ORIGIN
Query Match      6.7%; Score 78.8; DB 13; Length 410;
Best Local Similarity 55.0%; Pred. No. 5.1e-09;
Matches 177; Conservative 0; Mismatches 142; Indels 3; Gaps 1;

QY 53 TGGCAATTTTAAAGTCTTCATTTGGCTTGTATATAGTAGGCAATGCTGTGGTCACT 112
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21 TTGTAATTAATTGGATTAATTTTCTCATTAGCTACAAAGATCGGAATGCTCTTGTATGC 80

QY 113 TAGCCCTTTGGTGACAGAACCTTAGACATCGAAGTAATTAATTTTCTTAATTCGG 172
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
81 TTTCTAATTTGTGTGATATAAAATACAAACAATTAGCAATTAATTTCTTTCTCTTAG 140

QY 173 CTATTTCTGACTTCCTCGTGGGTTTGATTTCATTCCTCTGTACATCCCTCACGTTTGT 232
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
141 CTGTTGCTGATCTTACTATTGGCTTAATTTCTATTCCTCTTATGACTTTATATACGGCA 200

QY 233 TTAACT---TGGAAATTTGGAAGTGAATCTGCAAGTTTGGCTCAATTAATGCTATCTTT 289
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
201 ATGAGACTTGGACTTTTGGTTATTTCTTTGTCAATTCGGCTCTGTATAGATTATTTAA 260

QY 290 TGTGCAACGCTCTGTCTAGCAATATTGTCCTCATTAAGTACGATCGATACCACTCAGTTT 349
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
261 TGTGCAATGCTTCAGCACTCAATTTGTTATTAAATTAGCTTTGATAGATACTTTTCTGTTA 320

QY 350 CAAATGCTGTCTTCTTATAGGGC 371
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
321 CCCGACCTTTAACTTACAGGCC 342

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RESULT 15
BJ122942
LOCUS      523 bp      mRNA      linear      EST 23-JAN-2002
DEFINITION BJ122942 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1293h04 5', mRNA sequence.
ACCESSION  BJ122942
VERSION    BJ122942.1 GI:18283081
KEYWORDS
SOURCE
ORGANISM  Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 523)
Kohara,Y., Shin-I., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2002)
Contact: Tadasi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .523
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1293h04"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"

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FEATURES
source
1. .523
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1293h04"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"

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ORIGIN
Query Match      6.4%; Score 75.8; DB 12; Length 523;
Best Local Similarity 55.0%; Pred. No. 3.1e-08;

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Matches	171;	Conservative	0;	Mismatches	137;	Indels	3;	Gaps	1;
QY	73	TTTGCTTTGCTATATGTTAGCAATGCTGGTCATCTTAGCCCTTTGCTGGTGACAGA	132						
Db	78	TTGCGATTAGTAACCTCACTTGGAAATTTGATGGTAATGGTTAGCTTCAAAATCGACAAG	137						
QY	133	AACCTTAGACATCGAAGTAATTTTCTTAAATTTGGCTATTCTGACTTCCTCGTG	192						
Db	138	CAACTTCAGACAATTTAGTAACTATTCTCTGTTTAGCCGTCGCAGATATTGCAATT	197						
QY	193	GGTTTGATTTCCATTCTCTGTACATCCCTCAC---GTGTTGTTTAACTGGAATTTTGA	249						
Db	198	GGTGTCAATCAATACCCATGTTACATATACACTGCAATTCAAAAATGGGATCTTGA	257						
QY	250	AGTGGAACTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGACCGCATCTGTCTAC	309						
Db	258	TACACAATGTGCCAGTCTGGTTATGTCATCGATTATTTAATGAGCAACGACCGCTCCTG	317						
QY	310	AATATTGCTCTCATTAGTAGTACGATCGATCCAGTTCAGTTTCAAATGCTGTGCTTATAGG	369						
Db	318	AATCTTCTGCTCATTTTCTTCCCTCGATCGATCTCTCTAGTGACACGACCGTTGCTACAGG	377						
QY	370	GCTCAACACAC	380						
Db	378	CCTAGAAGAAC	388						

Search completed: October 1, 2004, 13:52:37  
 Job time : 3526 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 13:54:44 ; Search time 4880 Seconds  
(without alignments)  
10444.961 Million cell updates/sec

Title: US-10-626-445-5  
Perfect score: 1176  
Sequence: 1 atgtcggagttaacagttac.....accagtcagttcttcttga 1176

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb.pa.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rod.\*
- 36: em.htg.man.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1176	100.0	1538	10	AF358859	Mus muscu
c	819	69.6	200346	2	AC131672	AC131672 Mus muscu
3	67	5.7	1593	10	AF358860	AF358860 Rattus no
c	67	5.7	236694	2	AC118386	AC118386 Rattus no
5	28	2.4	1291	4	AB053300	AB053300 Sus scro
6	26	2.2	1451	10	AF358858	AF358858 Cavia por
7	22	1.9	223	6	AX775381	AX775381 Sequence
8	22	1.9	849	11	BV056167	BV056167 S212P6390
9	22	1.9	1173	6	AR142850	AR142850 Sequence
10	22	1.9	1173	6	AR391860	AR391860 Sequence
11	22	1.9	1173	6	AX109119	AX109119 Sequence
12	22	1.9	1173	6	AX139113	AX139113 Sequence
13	22	1.9	1173	6	AX301763	AX301763 Sequence
14	22	1.9	1173	6	BD015847	BD015847 Novel pol
15	22	1.9	1173	9	AF307973	AF307973 Homo sapi
16	22	1.9	1173	9	AF325356	AF325356 Homo sapi
17	22	1.9	1173	9	AF329449	AF329449 Homo sapi
18	22	1.9	1173	9	AY008280	AY008280 Homo sapi
19	22	1.9	1173	9	AI136745	AI136745 Homo sapi
20	22	1.9	1173	9	HS298292	HS298292 Homo sapi
21	22	1.9	1227	6	BD097512	BD097512 Novel gua
22	22	1.9	1265	9	AB044934	AB044934 Homo sapi
23	22	1.9	1266	6	AX376577	AX376577 Sequence
24	22	1.9	1300	6	AX301229	AX301229 Sequence
25	22	1.9	1312	6	BD095598	BD095598 Novel gua
26	22	1.9	1312	9	AB045370	AB045370 Homo sapi
27	22	1.9	3689	6	AX549343	AX549343 Sequence
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29	22	1.9	91811	10	AL670670	AL670670 Mouse DNA
c	22	1.9	140555	9	AC007922	AC007922 Homo sapi
31	22	1.9	168206	2	AC009668	AC009668 Homo sapi
c	22	1.9	167296	2	AF002507	AF002507 Homo sapi
33	22	1.9	169144	9	AC090244	AC090244 Homo sapi
c	22	1.9	184938	2	AP002476	AP002476 Homo sapi
35	22	1.9	193779	2	AP001327	AP001327 Homo sapi
c	22	1.9	229392	2	AC112372	AC112372 Rattus no
37	22	1.9	255561	2	AC121624	AC121624 Rattus no
c	21	1.8	358	4	AB060079	AB060079 Oryctolag
39	21	1.8	505	9	AF435588	AF435588 Homo sapi
40	21	1.8	696	6	AX677239	AX677239 Sequence
41	21	1.8	867	6	AR026630	AR026630 Sequence
42	21	1.8	1050	6	E12845	E12845 cDNA encodi
43	21	1.8	1250	9	AB029932S2	AB029933 Homo sapi
44	21	1.8	7019	9	AB009811	AB009811 Homo sapi
45	21	1.8	62240	2	AC100874	AC100874 Homo sapi

ALIGNMENTS

RESULT 1  
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LOCUS AF358859 1538 bp mRNA linear ROD 02-SEP-2001  
DEFINITION Mus musculus histamine H4 receptor mRNA, complete cds.  
ACCESSION AF358859  
VERSION AF358859.1 GI:15420534  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Comparison of human, mouse, rat, and guinea pig histamine H4  
receptor suggests substantial species variation

JOURNAL		Unpublished
REFERENCE		2. (bases 1 to 1538)
AUTHORS		Liu,C., Wilson,S., Kuei,C. and Lovenberg,F.W.
TITLE		Direct Submission
JOURNAL		Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA
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ORIGIN		
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Best Local Similarity		100.0%; Pred. No. 0;
Matches 1176; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
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QY	61	TTAATGCTTCATTTCGCTTTGCTAATAAGTAGGCAATGCTGTGGTCATCTTAGCCTTT 120
DB	121	TTAATGCTTCATTTCGCTTTGCTAATAAGTAGGCAATGCTGTGGTCATCTTAGCCTTT 180
QY	121	GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
DB	181	GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 240
QY	181	GACTTCCTCGTGGTTGATTTCCATCTCTGTACATCCCTCACGCTGTTTAACTGG 240
DB	241	GACTTCCTCGTGGTTGATTTCCATCTCTGTACATCCCTCACGCTGTTTAACTGG 300
QY	241	AAATTTTGAAGTGGAACTCTGCATGTTTGGCTCAATTAAGTACTATCTTTTGTGACCGCA 300
DB	301	AAATTTTGAAGTGGAACTCTGCATGTTTGGCTCAATTAAGTACTATCTTTTGTGACCGCA 360
QY	301	TCGTCTTACAAATATGTCCTCAATAGTACATGATGATACGATCAGTCTCAATGCTGTG 360
DB	361	TCGTCTTACAAATATGTCCTCAATAGTACATGATGATACGATCAGTCTCAATGCTGTG 420
QY	361	TCATTATAGGCTCAACACATGCGATCATGAGATTTGCTCAAAATGGTGGCTTTTGG 420
DB	421	TCATTATAGGCTCAACACATGCGATCATGAGATTTGCTCAAAATGGTGGCTTTTGG 480
QY	421	ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCGGCTTCAGATTTCTTGAAGAAGCAGC 480
DB	481	ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCGGCTTCAGATTTCTTGAAGAAGCAGC 540
QY	481	ACGAACACAAAGGACTGTGAGCTTGGTTTACAGATGATACATCTCACCATTACA 540
DB	541	ACGAACACAAAGGACTGTGAGCTTGGTTTACAGATGATACATCTCACCATTACA 600
QY	541	ATGCTCTTGAATTCCTGCTTCCTGTCATCTCTGGCTTATTTCAATGTACAGATTTC 600
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QY	601	TGGAGCCTGTGGAAGCGTAGGGCTCTCTAGTAGGTGGCCCTAGCCATGCTGGATTCTCCACT 660

DB	661	TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGTGCCTTAGCCATGCTGATTTCCACT 720
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QY	721	CCTGATTTGAAGGAATCAGTGCATCTCTCCTCACTCAGAAAGTCTCTGAAAGAGACAGC 780
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QY	781	ATCCTGGTGTCTTAAAGGACTCAGTGAACACAGATATCAGTCCCTTCAAAGTGGGTTC 840
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QY	1021	TGCTACAGCATTCCTTCTGCGTGCATGTTCAATTCGTTTGAATCCCTTCTGTAC 1080
DB	1081	TGCTACAGCATTCCTTCTGCGTGCATGTTCAATTCGTTTGAATCCCTTCTGTAC 1140
QY	1081	CTTTTGTGTACAGGCGTTTCCAGAAAGGCTTTCTGAAAGATCTTTGTGTGACAAAGCAA 1140
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QY	1141	CCAGCGCTGTACAGAACCAAGTCAGTATCTTCTTGA 1176
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RESULT 2

AC131672/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AC131672 200346 bp DNA linear HTG 06-NOV-2003

Mus musculus chromosome UNK clone RP23-314021, WORKING DRAFT

SEQUENCE, 4 unordered pieces.

AC131672.2 GI:38194370

HTG; HTGS\_PHASE1; HTGS\_DRAFT.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 200346)

Wilson,R.K.

The sequence of Mus musculus clone

Unpublished

2 (bases 1 to 200346)

McPherson,J.D. and Waterston,R.H.

Direct Submission

Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

3 (bases 1 to 200346)

Wilson,R.K.

Direct Submission

Submitted (06-NOV-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

On Nov 6, 2003 this sequence version replaced gi:22475584.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu>

Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)





NLRHSNYFFFLNLAISDFVGVISIPLYPIHTLFNNFSGICMFWLITDYLLCTASV  
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 IATSRGTHSARTGLACTSLPGKPEAASHSPSPGKSSLLVSLRTHMSGSLIAF  
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## ORIGIN

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QY 290 TGTGCAC 296  
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Db 325 TGTGCAC 331  
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## RESULT 4

AC118386/c

LOCUS

DEFINITION

AC118386 236694 bp DNA linear HTG 15-NOV-2002  
 Rattus norvegicus clone CH230-397N16, \*\*\* SEQUENCING IN PROGRESS

\*\*\*, 3 unordered pieces.

AC118386

AC118386.4

GI:25013229

HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 236694)

Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,

Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,

Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,

Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,

Biswal,O., Blair,J.J., Blankenburg,K., Blyth,P., Brown,M.,

Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,

Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Chen,A.,

Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,

Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,

Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,

Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Dixya,K.,

Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,

Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,

Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,

Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,

Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,

Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,

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Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hoques,M.,

Hollins,B., Howells,L., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,

Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,

Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,

Kowis,C., Kraft,C.I., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,

Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,

Lorensuhewa,L., Louisedge,H., Lozado,R.J., Lu,X., Ma,J.,

Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,

Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,

Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,

Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,

Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,

Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,

Nwaokeleneh,O., Okwuonu,G., Olarnpusagoon,A., Pal,S., Parks,K.,

Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,

Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,

Pruzo,M., Quirez,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,

Reilly,B., Reilly,N., Ren,Y., Reuter,M., Richards,S., Riggs,F.,

Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,

Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,

## TITLE

JOURNAL

REFERENCE

AUTHORS

JOURNAL

TITLE

JOURNAL

REFERENCE

AUTHORS

JOURNAL

TITLE

JOURNAL

REFERENCE

AUTHORS

JOURNAL

COMMENT

Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,  
 Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,  
 Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,  
 Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,  
 Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,  
 Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,  
 Williams,G., Willison,R., Wleczyk,R., Wooden,H., Worley,K.,  
 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,  
 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von  
 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
 Weinstein,G. and Gibbs,R.A.

Direct Submission

Unpublished

2 (bases 1 to 236694)

Worley,K.C.

Direct Submission

Submitted (17-APR-2002)

Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 236694)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23812823.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GUEK  
 Center clone name: CH230-397N16  
 ----- Summary Statistics  
 Assembly program: Phrap, version 0.990329  
 Consensus quality: 175902 bases at least Q40  
 Consensus quality: 179521 bases at least Q30  
 Consensus quality: 181489 bases at least Q20  
 Estimated insert size: 182948; sum-of-contigs estimation  
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length  
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).

----- NOTE: This is a 'working draft' sequence. It currently  
 consists of 3 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.

----- This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 217900: contig of 217900 bp in length  
 217901 218000: gap of unknown length  
 218001 234816: contig of 16816 bp in length  
 234817 234917: gap of unknown length  
 234917 236694: contig of 1778 bp in length.

Location/Qualifiers  
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 /mol\_type="genomic DNA"

FEATURES  
 source

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2310..3895
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120992..122993
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clone_end:Sp6
site:
end sequence:BZ179483"
210891..213141
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216516..217900
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.9e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 TGTTAACTGGAATTTGGAAGTGAATCTGCATGTTTGGCTCACTACTATCTTT 289
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QY 290 TGTGCAC 296
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Db 190225 TGTGCAC 190219

RESULT 5
AB053300
LOCUS      AB053300                1291 bp mRNA linear MAM 21-MAY-2002
DEFINITION Sus scrofa mRNA for histamine H4 receptor, complete cds.
ACCESSION  AB053300
VERSION     AB053300.1 GI:18147216
KEYWORDS
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
REFERENCE   1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
            Oda,T., Matsumoto,S., Masuho,Y., Takasaki,J., Matsumoto,M.,
            Kamohara,M., Saito,T., Ohishi,T., Soga,T., Hiyama,H., Matsushime,H.
            and Furuichi,K.
            cDNA cloning and characterization of porcine histamine H4 receptor
            Biochim. Biophys. Acta 1575 (1-3), 135-138 (2002)
            22015261
            PUBMED
            2 (bases 1 to 1291)
            Matsumoto,S., Oda,T. and Saito,Y.
            Direct Submission
            Submitted (08-JAN-2001) Shunichiro Matsumoto, Yamanouchi
            Pharmaceutical Co., Ltd., Institute for Drug Discovery Research; 21
            Miyukigaoka, Tsukuba, Ibaraki 305-8585, Japan
            (E-mail:matsumot@yamanouchi.co.jp, Tel:81-298-54-1610,
            Fax:81-298-52-5444)
            Location/Qualifiers
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CDS

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QGQDCPFGFLKGYVLAITLFFFLAPVLLVAYFNLYIYMSLWKRHLRSCQSGCL
TPVSSGSGHSGFRGLFSRTSLSDPKAAASLHSEPRRSTLWFLRTRMSLTSAN
KGLSHSDSLALHOKHELELLRAKLARSALAILLGVFAICWAPYSLLITFESVPTNP
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Query Match      2.4%; Score 28; DB 4; Length 1291;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 AAACCTTAGACATCGAAGTAATTTATTTT 159
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Db 201 AAACCTTAGACATCGAAGTAATTTATTTT 228
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RESULT 6
AF358858
LOCUS      AF358858                1451 bp mRNA linear ROD 02-SEP-2001
DEFINITION Cavia porcellus histamine H4 receptor mRNA, complete cds.
ACCESSION  AF358858
VERSION     AF358858.1 GI:15420532
KEYWORDS
SOURCE      Cavia porcellus (domestic guinea pig)
ORGANISM    Cavia porcellus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
            Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
            Comparison of human, mouse, rat, and guinea pig histamine H4
            receptor suggests substantial species variation
            Unpublished
            2 (bases 1 to 1451)
            Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
            Direct Submission
            Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
            Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
            CA 92121, USA
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Query Match      2.2%; Score 26; DB 10; Length 1451;
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 TTTTGGCTCACTACTGACTATCTTTT 290
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RESULT 7
AX775381
LOCUS      AX775381                223 bp DNA linear PAT 09-JUL-2003

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DEFINITION Sequence 697 from Patent WO03038129.  
ACCESSION AX775381  
VERSION AX775381.1 GI:32486897  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Raponi,M.  
TITLE Methods for assessing and treating leukemia  
JOURNAL Patent: WO 03038129-A 697 08-MAY-2003;  
Ortho-Clinical Diagnostics, Inc. (US)  
FEATURES  
source  
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Query Match 1.9%; Score 22; DB 6; Length 223;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 966 TCTGTTCACAATTGTCCTTTCA 987  
Db 197 TCTGTTCACAATTGTCCTTTCA 218  
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BV056167 849 bp DNA linear STS 31-MAY-2003  
LOCUS S212P6390PD12.T0 CZECHII/Ei Mus musculus STS genomic, sequence  
DEFINITION tagged site.  
ACCESSION BV056167  
VERSION BV056167.1 GI:31171962  
KEYWORDS STS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Lander,E.S., Kulkobas,E.J. III, Kirby,A.W., Zody,M.C., Mullikin,J.C.,  
Wade,C.M., Lindblad-Toh,K. and Daly,M.J.  
TITLE The mosaic structure of variation in the laboratory mouse genome  
JOURNAL Nature 420 (6915), 574-578 (2002)  
MEDLINE 22354684  
PubMed 12466852  
COMMENT Contact: Kerstin Lindblad-Toh  
Whitehead Institute for Biomedical Research, Center for Genome  
Research  
320 Charles Street, Cambridge, MA 02141, USA  
Tel: 6172521477  
Fax: 6172580903  
Email: kersli@genome.wi.mit.edu  
Primer A: None  
Primer B: None  
STS size: 849  
Protocol:  
WGS-discovery: Paired-end low-coverage whole genome shotgun reads  
were generated from 129S1/SvimJ, C3H/HeJ, and BALB/cByJ. The WGS  
reads were placed uniquely on the MGSv3 C57BL/6J assembly and SNP  
detection was carried out by SSAHA-SNP. 225,000 reads were  
annotated  
as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J  
and the strain from which the particular read came. The validation  
rate for these SNPs was estimated at approximately 98%.  
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 266 GCTTCTGTCATCTCTGTGGCT 287  
RESULT 9  
AR142850 1173 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 1 from patent US 6204017.  
DEFINITION AR142850  
ACCESSION AR142850  
VERSION AR142850.1 GI:15104136  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1173)  
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,  
Umland,S.P. and Wang,S.  
TITLE Polynucleotide encoding a histamine receptor  
JOURNAL Patent: US 6204017-A 1 20-MAR-2001;  
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QY 966 TCTGTTCACAATTGTCCTTTCA 987  
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AR391860 1173 bp DNA linear PAT 18-DEC-2003  
LOCUS Sequence 1 from patent US 6613533.  
DEFINITION AR391860  
ACCESSION AR391860  
VERSION AR391860.1 GI:40115588  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1173)  
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,  
Umland,S.P. and Wang,S.  
TITLE Histamine receptor  
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;  
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Db 960 TCTGTTCACAATTGTCCTTTCA 981

RESULT 11  
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LOCUS AX109119 1173 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 1 from Patent WO0125432.  
ACCESSION AX109119  
VERSION AX109119.1 GI:13924093  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L.,  
Umland, S. and Wang, S.  
TITLE Histamine receptor  
JOURNAL Patent: WO 0125432-A 1 12-APR-2001;  
SCHERING CORPORATION (US)  
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DEFINITION Sequence 1 from Patent EP1096009.  
ACCESSION AX139113  
VERSION AX139113.1 GI:14274791  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Peter, B. and O'Reilly, M.A.  
TITLE G-protein coupled receptor-like polypeptide  
JOURNAL Patent: EP 1096009-A 1 02-MAY-2001;  
Pfizer Limited (GB); PFIZER INC. (US)  
FEATURES  
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LOCUS AX301763 1173 bp DNA linear PAT 30-NOV-2001  
DEFINITION Sequence 1 from Patent WO0185786.  
ACCESSION AX301763  
VERSION AX301763.1 GI:17382844

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Jones, P.G., Blatcher, M., Wu, S. and Pausch, M.H.  
TITLE Human histamine h42 receptor  
JOURNAL Patent: WO 0185786-A 1 15-NOV-2001;  
American Home Products Corporation (US)  
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Db 960 TCTGTTCCAAATTCCTCTTCA 981  
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LOCUS BD015847 1173 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel polypeptide.  
ACCESSION BD015847  
VERSION BD015847.1 GI:22556984  
KEYWORDS JP 2001211889-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1173)  
Peter, B. and Olaylee, M.A.  
TITLE Novel polypeptide  
JOURNAL Patent: JP 2001211889-A 1 07-AUG-2001;  
PFIZER INC  
COMMENT OS Homo sapiens (human)  
PN JP 2001211889-A/1  
PD 07-AUG-2001  
PR 27-OCT-2000 JP 2000329359  
PR 29-OCT-1999 GB 9925641:4, 20-APR-2000 GB 0009973:9 PI  
BEAT PETER, MARK ANTONY OLAYLEE  
PC C12N15/09, A61K38/00, A61K39/395, A61K48/00, A61P1/04,  
PC A61P11/00,  
PC A61P11/06, A61P29/00, A61P31/00, A61P35/00, A61P37/02, A61P37/08,  
PC C07K14/00,  
PC C07K14/705, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/PC  
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PC C12N15/00,  
PC A61K37/02, C12N5/00  
CC Novel polypeptide  
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QY 966 TCTGTTCAAAATGTCCTTTCA 987  
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Db 960 TCTGTTCAAAATGTCCTTTCA 981

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LOCUS AF307973 1173 bp mRNA linear PRI 14-NOV-2000  
DEFINITION Homo sapiens histamine H4 receptor mRNA, complete cds.  
ACCESSION AF307973  
VERSION AF307973.1 GI:11141732  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Jones, P.G., Wu, S. and Betty, M.  
TITLE Cloning of a novel histamine receptor  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1173)  
AUTHORS Jones, P.G., Wu, S. and Betty, M.  
TITLE Direct Submission  
JOURNAL Submitted (25-SEP-2000) Neuroscience, Wyeth Ayerst, CN8000,  
Princeton, NJ 08543, USA  
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Title: US-10-626-445-5

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- 10: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1176	100.0	1176	6	AAI70981 Mouse his
2	67	5.7	1176	6	AAI70982 Rat hista
3	30	2.6	30	6	AAI70992 Mouse his
4	29	2.5	29	6	AAI70991 Mouse his
5	26	2.2	1170	6	AAI70983 Guinea pi
6	23	2.0	39	6	AAI70993 Mouse his
7	22	1.9	223	9	Ade85481 Farnesyl
8	22	1.9	540	6	AAI70981 Mouse his
9	22	1.9	1103	8	AAI70982 Rat hista
10	22	1.9	1166	8	AAI70982 Rat hista
11	22	1.9	1170	8	AAI70982 Rat hista
12	22	1.9	1173	3	AAI70982 Rat hista
13	22	1.9	1173	3	AAI70982 Rat hista
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16	22	1.9	1173	6	AAI70982 Rat hista
17	22	1.9	1173	6	AAI70982 Rat hista
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19	22	1.9	1173	6	AAI70982 Rat hista
20	22	1.9	1173	6	AAI70982 Rat hista
21	22	1.9	1173	7	AAI70982 Rat hista
22	22	1.9	1227	4	AAI70982 Rat hista
23	22	1.9	1265	6	AAI70982 Rat hista

24	22	1.9	1265	8	AAI70982 Rat hista
25	22	1.9	1266	6	AAI70982 Rat hista
26	22	1.9	1300	6	AAI70982 Rat hista
27	22	1.9	1312	4	AAI70982 Rat hista
28	22	1.9	3689	7	AAI70982 Rat hista
29	21	1.8	696	7	AAI70982 Rat hista
30	21	1.8	867	2	AAI70982 Rat hista
31	21	1.8	1050	2	AAI70982 Rat hista
32	21	1.8	220895	6	AAI70982 Rat hista
33	20	1.7	348	4	AAI70982 Rat hista
34	20	1.7	536	4	AAI70982 Rat hista
35	20	1.7	693	7	AAI70982 Rat hista
36	20	1.7	693	7	AAI70982 Rat hista
37	20	1.7	867	4	AAI70982 Rat hista
38	20	1.7	1053	2	AAI70982 Rat hista
39	20	1.7	1085	2	AAI70982 Rat hista
40	20	1.7	1085	7	AAI70982 Rat hista
41	20	1.7	1149	2	AAI70982 Rat hista
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#### ALIGNMENTS

#### RESULT 1

ID AAI70981 standard; cDNA; 1176 BP.  
XX  
AC AAI70981;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Mouse histamine H4 receptor cDNA.  
XX  
KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy; ss.  
XX  
OS Mus musculus.  
XX  
FN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Lovenberg T, Liu C;  
XX  
DR WPI; 2002-114339/15.  
XX  
P-ESDB; AAMS0565.  
XX  
New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.  
XX  
Claim 4; Fig 5A; 92pp; English.  
XX  
The present sequence is that of a cDNA clone encoding a murine histamine receptor of the H4 subtype. The cDNA was isolated from a mouse spleen cDNA library. It shows 72.8% homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAMS0564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of

CC diseases where it is beneficial to elevate mammalian histamine H4  
CC receptor activity. Recombinant protein is useful for identifying  
CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
CC useful for diagnosing, treating or preventing asthma, allergy,  
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
CC disorders of the neuroendocrine system, stress and spasticity  
XX  
SQ Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1176; DB 6; Length 1176;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGTCCCTTGGCATTT 60  
DB 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGTCCCTTGGCATTT 60  
QY 61 TTAATGCTCTTCAATTCGCTTTGTATAATGGTAGGCAATGCTGTGTCATCTTAGCCTTT 120  
DB 61 TTAATGCTCTTCAATTCGCTTTGTATAATGGTAGGCAATGCTGTGTCATCTTAGCCTTT 120  
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTTCTTAATTTGGCTATTCT 180  
DB 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTTCTTAATTTGGCTATTCT 180  
QY 181 GACTTCTGTGGGTTGATTTCATTCCATCTCTGTACATCCCTCAGTGTGTTAACTGG 240  
DB 181 GACTTCTGTGGGTTGATTTCATTCCATCTCTGTACATCCCTCAGTGTGTTAACTGG 240  
QY 241 AATTTTGGAGTGGAAATCTGATGTTTGGCTCAATTAATCTGATCTTTTGTGCACCGCA 300  
DB 241 AATTTTGGAGTGGAAATCTGATGTTTGGCTCAATTAATCTGATCTTTTGTGCACCGCA 300  
QY 301 TCTGTCTACAAATATGTCCTCAATAGTACGATCGATACCAAGTCAAGTTCAAAATGCTGTG 360  
DB 301 TCTGTCTACAAATATGTCCTCAATAGTACGATCGATACCAAGTCAAGTTCAAAATGCTGTG 360  
QY 361 TCTTATAGGCTCAACACATGCGATCATGAAGATGTTGCTCAAAATGCTGTGTTGG 420  
DB 361 TCTTATAGGCTCAACACATGCGATCATGAAGATGTTGCTCAAAATGCTGTGTTGG 420  
QY 421 ATACTGGCTTTCTTGGTAAATGCGCGATGATTTCTGGCTTCAGATTTCTTGGAAAGAACAGC 480  
DB 421 ATACTGGCTTTCTTGGTAAATGCGCGATGATTTCTGGCTTCAGATTTCTTGGAAAGAACAGC 480  
QY 481 ACGAACAAAGAGCTGTGAGCTGTGGCTTTGTGTACAGAGTGTATCCTCAACATTACA 540  
DB 481 ACGAACAAAGAGCTGTGAGCTGTGGCTTTGTGTACAGAGTGTATCCTCAACATTACA 540  
QY 541 ATGCTCTTGAATTCCTGCTTCTGTCATCTCTGCTTATTTCAATGTACAGATTAC 600  
DB 541 ATGCTCTTGAATTCCTGCTTCTGTCATCTCTGCTTATTTCAATGTACAGATTAC 600  
QY 601 TGGAGCTGTGGAAAGCTAGGCTCTCAGTAGGTGCGCTAGCCATGCTGGATTCTCCACT 660  
DB 601 TGGAGCTGTGGAAAGCTAGGCTCTCAGTAGGTGCGCTAGCCATGCTGGATTCTCCACT 660  
QY 661 ACCTCTTCCAGTGTCTCAGGACATTTACAGAGCTGGGTGGCTTCGAGGACAAGTAAT 720  
DB 661 ACCTCTTCCAGTGTCTCAGGACATTTACAGAGCTGGGTGGCTTCGAGGACAAGTAAT 720  
QY 721 CCTGGATTGAGGAATCAGTGTGATCTCGTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780  
DB 721 CCTGGATTGAGGAATCAGTGTGATCTCGTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780  
QY 781 ATCTGTGTCTTAAAGACTTCACATGAACAGAGTATCACTGCTCTCAAAGTGGTTC 840  
DB 781 ATCTGTGTCTTAAAGACTTCACATGAACAGAGTATCACTGCTCTCAAAGTGGTTC 840  
QY 841 TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGAGAGCTTCTCAGAGGC 900  
DB 841 TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGAGAGCTTCTCAGAGGC 900

QY 901 AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTCCCATTTCTGGGTCCA 960  
DB 901 AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTCCCATTTCTGGGTCCA 960  
QY 961 TACTGTCTGTTTCAATTTGCTTCTTCAATTTGCTTCTTCAATTTGCTTCTTCAATTTGCTTCT 1020  
DB 961 TACTGTCTGTTTCAATTTGCTTCTTCAATTTGCTTCTTCAATTTGCTTCTTCAATTTGCTTCT 1020  
QY 1021 TGGTACAGCATTTGCCCTTCTGCTGCAATGTTCAATTTGTTTAAATCCCTTCTCTGTAC 1080  
DB 1021 TGGTACAGCATTTGCCCTTCTGCTGCAATGTTCAATTTGTTTAAATCCCTTCTCTGTAC 1080  
QY 1081 CTTTGTGTGTCACAGGCTTTTCCAGAGGCTTTTCTGGAAGATATCTTTGTGTGACAAAGCAA 1140  
DB 1081 CTTTGTGTGTCACAGGCTTTTCCAGAGGCTTTTCTGGAAGATATCTTTGTGTGACAAAGCAA 1140  
QY 1141 CCAGCGCTGTACAGAACCCAGTCAGTATCTTCTTGA 1176  
DB 1141 CCAGCGCTGTACAGAACCCAGTCAGTATCTTCTTGA 1176

RESULT 2

AAI70982  
ID AAI70982 standard; cDNA; 1176 BP.  
XX  
AC AAI70982;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Rat histamine H4 receptor cDNA.  
XX  
KW Histamine H4 receptor; rat; antiallergic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy; ss.  
XX  
OS Rattus rattus.  
XX  
PN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US0005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Lovenberg T, Liu C;  
XX  
PI WPI; 2002-114339/15.  
XX  
PI P-PSDB; AAM50566.  
XX  
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
PT the proteins, useful in gene therapy for treating diseases where it is  
PT beneficial to elevate mammalian histamine H4 receptor activity.  
XX  
PS Claim 4; Fig 5C; 92pp; English.  
XX  
CC The present sequence is that of a cDNA clone encoding a rat histamine  
CC receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA  
CC library. It shows 72.5% homology to the human H4 receptor coding region.  
CC The invention provides mammalian (human, mouse, rat and guinea pig)  
CC histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
CC recombinant host cells that produce active recombinant protein. The  
CC pharmacology of known histamine ligands is demonstrated. Mammalian  
CC histamine H4 receptor may be used in gene therapy for the treatment of  
CC diseases where it is beneficial to elevate mammalian histamine H4  
CC receptor activity. Recombinant protein is useful for identifying  
CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
CC useful for diagnosing, treating or preventing asthma, allergy,  
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin



CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity  
 XX Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;  
 SQ Query Match 5.7%; Score 67; DB 6; Length 1176;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-23;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 TGTAACTGGAATTTTGGAGTGGAACTGCAATGTTTGGCTCATCTACTGACTATCTTT 289  
 DB 230 TGTAACTGGAATTTTGGAGTGGAACTGCAATGTTTGGCTCATCTACTGACTATCTTT 289

QY 290 TGTGCAC 296  
 DB 290 TGTGCAC 296

RESULT 3  
 AAI70992  
 ID AAI70992 standard; DNA; 30 BP.  
 AC AAI70992;  
 XX  
 DT 18-MAR-2002 (first entry)  
 XX  
 DE Mouse histamine H4 receptor gene specific primer P2.  
 XX  
 KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy; PCR primer; RACE; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200192485-A1.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 22-FEB-2001; 2001WO-US005914.  
 XX  
 PR 31-MAY-2000; 2000US-0208260P.  
 XX  
 PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
 XX  
 PI Lovenberg T, Liu C;  
 XX  
 DR WPI; 2002-114339/15.  
 XX  
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 PS Example 10; Page 48; 92pp; English.  
 XX  
 CC The present sequence is that of mouse histamine H4 receptor gene specific  
 CC primer P2, which was used with an adaptor primer (see AAI70990) in a 3',  
 CC RACE amplification of mouse spleen cDNA. Full-length cDNA (see AAI70981)  
 CC encoding mouse H4 (see AAM50565) was subsequently obtained. The invention  
 CC provides mammalian histamine H4 receptor nucleic acid molecules and  
 CC polypeptides. The nucleic acids have been expressed in recombinant host  
 CC cells that produce active recombinant protein. Mammalian histamine H4  
 CC receptor may be used in gene therapy for the treatment of diseases where  
 CC it is beneficial to elevate mammalian histamine H4 receptor activity.  
 CC Recombinant H4 receptor protein can be used to identify modulators of  
 CC activity for use in the treatment of asthma, allergy, inflammation,  
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
 CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
 CC the neuroendocrine system, stress and spasticity  
 XX  
 SQ Sequence 30 BP; 8 A; 9 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 2.6%; Score 30; DB 6; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 0.00026;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 741 TGCATCTCGTCACTCAGAAAGTCTCGAAG 770  
 DB 1 TGCATCTCGTCACTCAGAAAGTCTCGAAG 30

RESULT 4  
 AAI70991/C  
 ID AAI70991 standard; DNA; 29 BP.  
 XX  
 AC AAI70991;  
 XX  
 DT 18-MAR-2002 (first entry)  
 XX  
 DE Mouse histamine H4 receptor gene specific primer P1.  
 XX  
 KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy; PCR primer; RACE; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200192485-A1.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 22-FEB-2001; 2001WO-US005914.  
 XX  
 PR 31-MAY-2000; 2000US-0208260P.  
 XX  
 PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
 XX  
 PI Lovenberg T, Liu C;  
 XX  
 DR WPI; 2002-114339/15.  
 XX  
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 PS Example 10; Page 48; 92pp; English.  
 XX  
 CC The present sequence is that of mouse histamine H4 receptor gene specific  
 CC primer P1, which was used with an adaptor primer (see AAI70990) in a 5',  
 CC RACE amplification of mouse spleen cDNA. Full-length cDNA (see AAI70981)  
 CC encoding mouse H4 (see AAM50565) was subsequently obtained. The invention  
 CC provides mammalian histamine H4 receptor nucleic acid molecules and  
 CC polypeptides. The nucleic acids have been expressed in recombinant host  
 CC cells that produce active recombinant protein. Mammalian histamine H4  
 CC receptor may be used in gene therapy for the treatment of diseases where  
 CC it is beneficial to elevate mammalian histamine H4 receptor activity.  
 CC Recombinant H4 receptor protein can be used to identify modulators of  
 CC activity for use in the treatment of asthma, allergy, inflammation,  
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
 CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
 CC the neuroendocrine system, stress and spasticity  
 XX  
 SQ Sequence 29 BP; 9 A; 10 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 2.5%; Score 29; DB 6; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 0.00081;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 493 GACTGTGAGCCTGGCTTTGTTACAGAGTG 521  
 DB 29 GACTGTGAGCCTGGCTTTGTTACAGAGTG 1

RESULT 5  
 AAI70983  
 ID AAI70983 standard; cDNA; 1170 BP.  
 XX

```
AC AAI70983;
XX
XX 18-MAR-2002 (first entry)
XX
DE Guinea pig histamine H4 receptor cDNA.
XX
XX Histamine H4 receptor; guinea pig; antiasthmatic; anti-allergenic;
KW antinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy; ss.
XX
OS Cavia porcellus.
XX
XX WO200192485-A1.
XX
XX 06-DEC-2001.
XX
XX 22-FEB-2001; 2001WO-US005914.
XX
XX 31-MAY-2000; 2000US-0208260P.
XX
XX (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
XX Lovenberg T, Liu C;
XX
XX WPI; 2002-114339/15.
XX
XX P-PSDB; AAM50567.
XX
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
XX Claim 4; Fig 6B; 92pp; English.
XX
XX The present sequence is that of a cDNA clone encoding guinea pig
CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone
CC marrow cDNA library. It shows 75.6% homology to the human H4 receptor
CC coding region. The invention provides mammalian (human, mouse, rat and
CC guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-
CC 83) and polypeptides (see AAM50564-67). The nucleic acids have been
CC expressed in recombinant host cells that produce active recombinant
CC protein. The pharmacology of known histamine ligands is demonstrated.
CC Mammalian histamine H4 receptor may be used in gene therapy for the
CC treatment of diseases where it is beneficial to elevate mammalian
CC histamine H4 receptor activity. Recombinant protein is useful for
CC identifying modulators of the mammalian histamine H4 receptor. Such
CC modulators may be useful for diagnosing, treating or preventing asthma,
CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-
CC insulin dependent diabetes mellitus, hyperglycemia, constipation,
CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity
XX
XX Sequence 1170 BP; 301 A; 286 C; 221 G; 362 T; 0 U; 0 Other;
SQ
Query Match 2.2%; Score 26; DB 6; Length 1170;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 265 TTTGGCTCATTACTGACTATCTTTT 290
DB 262 TTTGGCTCATTACTGACTATCTTTT 287
RESULT 6
AAI70993
ID AAI70993 standard; DNA; 39 BP.
XX
XX AAI70993;
XX
XX 18-MAR-2002 (first entry)
XX
XX Mouse histamine H4 receptor cDNA forward PCR primer.
DE
XX
XX Histamine H4 receptor; mouse; antiasthmatic; anti-allergenic;
KW antinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW
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```
KW diagnosis; gene therapy; PCR primer; ss.
XX
XX Mus musculus.
XX
XX WO200192485-A1.
XX
XX 06-DEC-2001.
XX
XX 22-FEB-2001; 2001WO-US005914.
XX
XX 31-MAY-2000; 2000US-0208260P.
XX
XX (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
XX Lovenberg T, Liu C;
XX
XX WPI; 2002-114339/15.
XX
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
XX Example 10; Page 49; 92pp; English.
XX
XX The present sequence is that of the forward primer used, with the reverse
CC primer given in AAI70994, in the PCR amplification of mouse spleen cDNA.
CC The coding region (see AAI70981) of mouse histamine H4 receptor cDNA was
CC obtained. The PCR product was cloned into mammalian expression vector
CC pcNeo. The invention provides mammalian histamine H4 receptor nucleic
CC acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The
CC nucleic acids have been expressed in recombinant host cells that produce
CC active recombinant protein. Mammalian histamine H4 receptor may be used
CC in gene therapy for the treatment of diseases where it is beneficial to
CC elevate mammalian histamine H4 receptor activity. Recombinant H4 receptor
CC protein can be used to identify modulators of activity for use in the
CC treatment of asthma, allergy, inflammation, cardiovascular and
CC cerebrovascular disorders, non-insulin dependent diabetes mellitus,
CC hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine
CC system, stress and spasticity
XX
XX Sequence 39 BP; 11 A; 10 C; 10 G; 8 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 23; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCGAGTCTAACAGTACTGG 23
DB 17 ATGTCGAGTCTAACAGTACTGG 39
RESULT 7
ADE85481
ID ADE85481 standard; DNA; 223 BP.
XX
XX ADE85481;
XX
XX 29-JAN-2004 (first entry)
XX
XX
XX
XX Farnesyl transferase inhibitor modulated leukemia associated gene #700.
DE ss; cytosstatic; farnesyl transferase inhibitor; gene expression;
KW quinolinone; leukemia; cancer.
XX
XX Homo sapiens.
XX
XX WO2003038129-A2.
XX
XX 08-MAY-2003.
XX
XX 30-OCT-2002; 2002WO-US034784.
XX
XX 30-OCT-2001; 2001US-0338997P.
XX
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PR 30-OCT-2001; 2001US-0340081P.
PR 30-OCT-2001; 2001US-0340938P.
PR 30-OCT-2001; 2001US-0341012P.
XX
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Raponi M;
XX
DR WPI; 2003-513497/48.
XX
PT Determining whether a patient will respond to treatment with a farnesyl
PT transferase inhibitor, by analyzing the expression of gene that is
PT differentially modulated in the presence of the inhibitor.
XX
PS Disclosure; SEQ ID NO 700; 346pp; English.
XX
CC The invention relates to a method of determining whether a patient will
CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC analyzing the expression of gene that is differentially modulated in the
CC presence of an FTI. The method is useful for determining whether a
CC patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC chlorophenyl)](1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
CC methyl-2-(1H)quinoline, monitoring the therapy of a patient, treating a
CC patient with leukemia with FTI if the analysis indicates that the patient
CC will respond. This sequence corresponds to a gene whose expression may be
CC modulated in the presence of FTI.
XX
SQ Sequence 223 BP; 57 A; 49 C; 43 G; 73 T; 0 U; 1 Other;

Query Match 1.9%; Score 22; DB 9; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTTCACAAATTGTCCTTTCA 987
Db 197 TCTGTTTCACAAATTGTCCTTTCA 218

RESULT 8
AAS98150/C
ID AAS98150 standard; DNA; 540 BP.
XX
AC AAS98150;
XX
XX
DT 12-MAR-2002 (first entry)
XX
DE Human DNA for potential G protein-coupled receptor #107.
XX
KW Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor;
KW Alzheimer's disease; amyotrophic lateral sclerosis; asthma;
KW atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;
KW chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
KW depression; epilepsy; macular degeneration; lymphoma; melanoma;
KW multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;
KW psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;
KW tuberculosis; cognition disorder; memory disorder; anorexia;
KW hormonal release disorder; cardiovascular activity disorder;
KW pain perception disorder; obesity; diabetes; diabetes;
KW hyperlipidaemia; stroke; gene therapy.
XX
OS Homo sapiens.
XX
XX
PN W0200185791-A1.
XX
XX
PD 15-NOV-2001.
XX
XX
PF 11-MAY-2001; 2001WO-US015332.
XX
XX
PR 11-MAY-2000; 2000US-0203217P.
XX
PR 18-MAY-2000; 2000US-0205945P.
XX
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
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PI Brown JP, Miller M, Burner G, Fabre-Suver C, Pritchard D;
XX
DR WPI; 2002-066595/09.
XX
PT Novel G protein-coupled receptor polypeptides including galanin receptor
PT polypeptides useful for identifying modulators that are useful for
PT treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,
PT stroke.
XX
XX
PS Claim 2; Page 106; 144pp; English.
XX
CC The invention relates to an isolated polypeptide encoded by a nucleic
CC acid molecule that is at least 80% identical to the G protein-coupled
CC (GPCR) polynucleotides included in the specification. Also included are
CC probes based on the GPCR sequences (including antisense probes), a host
CC cell comprising an expression vector comprising the GPCR sequence,
CC antibodies raised against the polypeptides, and methods of identifying
CC modulators of the polypeptides. The polypeptides are useful for
CC identifying modulator compounds which function as modulators, activators,
CC repressors, agonists or antagonists of the novel GPCR polypeptides
CC including the GAL4 polypeptide. The antibodies and nucleic acid probes as
CC described above can be used to detect the presence of the polypeptides
CC and nucleic acids and are used to diagnose a variety of diseases or
CC disorders in which GPCRs are involved e.g., Alzheimer's disease,
CC amyotrophic lateral sclerosis, asthma, atherosclerosis, basal cell
CC carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic
CC obstructive pulmonary disease, Crohn's disease, depression, epilepsy,
CC macular degeneration, lymphoma, melanoma, multiple sclerosis,
CC osteoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid
CC arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other
CC diseases listed in the specification. The probes and antibodies are also
CC useful for diagnosing cognition and memory disorders, anorexia, hormonal
CC release disorders, cardiovascular activity disorders, pain perception
CC disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds
CC that decrease or increase the expression of galanin receptor (GAL4) can
CC be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR
CC nucleic acid is useful for treating the above mentioned disorders by gene
CC therapy techniques. The present sequence is a novel GPCR polynucleotide
CC of the invention
XX
SQ Sequence 540 BP; 173 A; 107 C; 119 G; 138 T; 0 U; 3 Other;

Query Match 1.9%; Score 22; DB 6; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTTCACAAATTGTCCTTTCA 987
Db 173 TCTGTTTCACAAATTGTCCTTTCA 152

RESULT 9
AAS55123
ID AAD55123 standard; DNA; 1103 BP.
XX
AC AAD55123;
XX
XX
DT 07-AUG-2003 (first entry)
XX
DE Human H4 receptor splice variant (H4b) DNA.
XX
XX
KW Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;
KW atopic dermatitis; stroke; myocardial infarction; migraine; allergy;
KW chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;
KW rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;
KW asthma; receptor; variant; gene; ds.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 55..1065
FT /tag= a
FT /product= "Human H4b protein"
```



DR WPI; 2003-290186/28.  
 DR P-PSDB; AAE36417.  
 XX  
 PT Novel splice variants of human H4 histamine receptor, H4b and H4c, useful  
 for identifying agonists or antagonists of the receptor which are useful  
 for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.  
 PT  
 XX  
 PS Disclosure; Page 56-58; 31pp; English.  
 CC  
 CC The invention relates to splice variants of human H4 histamine receptor,  
 CC H4b and H4c. The invention is useful for identifying an agonist,  
 CC antagonist or inverse agonist of a mammalian histamine receptor. The  
 CC agonist, antagonist or inverse agonist of H4b and H4c is useful for  
 CC treating inflammation, asthma, allergy, atopic dermatitis, stroke,  
 CC myocardial infarction, migraine, chronic obstructive pulmonary disease  
 CC (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel  
 CC disease, or psoriasis. The present sequence is human H4 receptor DNA  
 XX  
 SQ Sequence 1170 BP; 292 A; 245 C; 231 G; 402 T; 0 U; 0 Other;  
 Query Match 1.9%; Score 22; DB 8; Length 1170;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 966 TCTGTTCAACAATTGTCCTTTCA 987  
 Db 960 TCTGTTCAACAATTGTCCTTTCA 981  
 RESULT 12  
 AAA46023  
 ID AAA46023 standard; cDNA; 1173 BP.  
 AC AAA46023;  
 XX  
 DT 22-AUG-2000 (first entry)  
 XX  
 DE Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13.  
 XX  
 KW Human; G protein coupled receptor; GPCR; transmembrane receptor;  
 KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WC200022131-A2.  
 PD 20-APR-2000.  
 XX  
 XX 13-OCT-1999; 99WO-US024065.  
 XX  
 PR 13-OCT-1998; 98US-00170496.  
 PR 12-NOV-1998; 98US-0108029P.  
 PR 20-NOV-1998; 98US-0109213P.  
 PR 27-NOV-1998; 98US-0110060P.  
 PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123944P.  
 PR 12-MAR-1999; 99US-0123945P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123948P.  
 PR 12-MAR-1999; 99US-0123949P.  
 PR 12-MAR-1999; 99US-0123951P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 28-MAY-1999; 99US-0137567P.  
 PR 29-JUN-1999; 99US-0141448P.  
 PR 27-AUG-1999; 99US-0151114P.  
 PR 03-SEP-1999; 99US-0152524P.  
 PR 29-SEP-1999; 99US-0156555P.

PR 29-SEP-1999; 99US-0156633P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 29-SEP-1999; 99US-0156653P.  
 PR 01-OCT-1999; 99US-0157280P.  
 PR 01-OCT-1999; 99US-0157281P.  
 PR 01-OCT-1999; 99US-0157282P.  
 PR 01-OCT-1999; 99US-0157293P.  
 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 PR 12-OCT-1999; 99US-00417044.  
 XX  
 PA (AREN-) ARENA PHARM INC.  
 XX  
 PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;  
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;  
 XX WPI; 2000-317986/27.  
 DR P-PSDB; AAB02831.  
 DR  
 XX Non-endogenous, human G protein-coupled receptors for screening receptor,  
 PT inverse or partial agonists useful as therapeutic agents.  
 XX  
 PS Example 1; Page 88-89; 187pp; English.  
 XX  
 CC The present invention describes transmembrane receptors, preferably human  
 CC protein coupled receptors (GPCR), for which the endogenous ligand is  
 CC unknown (orphan GPCR receptors). More specifically the present invention  
 CC relates to non-endogenous, constitutively activated versions of a human  
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct  
 CC identification of candidate compounds as receptors agonists, inverse  
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017  
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Query Match 1.9%; Score 22; DB 3; Length 1173;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 966 TCTGTTCAACAATTGTCCTTTCA 987  
 Db 960 TCTGTTCAACAATTGTCCTTTCA 981  
 RESULT 13  
 AAD01124  
 ID AAD01124 standard; cDNA; 1173 BP.  
 XX  
 AC AAD01124;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Human orphan G protein-coupled receptor hRUP7 cDNA.  
 XX  
 KW Human; orphan G protein-coupled receptor; GPCR; hRUP7; drug screening;  
 KW transmembrane receptor; signal cascade; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1173  
 FT /\*tag= a  
 FT /product= "hRUP7"  
 FT /note= "Human orphan G protein-coupled receptor"  
 XX  
 PN WC200031258-A2.  
 PD 02-JUN-2000.  
 XX  
 XX 13-OCT-1999; 99WO-US023687.  
 XX  
 PR 20-NOV-1998; 98US-0109213P.

PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123949P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.  
 PR 28-MAY-1999; 99US-0136567P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 29-JUN-1999; 99US-0141448P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156633P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 29-SEP-1999; 99US-0156653P.  
 PR 01-OCT-1999; 99US-0157280P.  
 PR 01-OCT-1999; 99US-0157281P.  
 PR 01-OCT-1999; 99US-0157282P.  
 PR 01-OCT-1999; 99US-0157293P.  
 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 PR 12-OCT-1999; 99US-00417044.  
 XX  
 PA (AREN-) ARENA PHARM INC.  
 XX  
 PI Chen R, Dang HT, Liaw CW, Lin I;  
 XX  
 DR WPI; 2000-400068/34.  
 DR P-PSDB; AAY71297.  
 XX  
 PT Novel human orphan G protein-coupled receptors and the encoding cDNAs for  
 PT use in the identification of G protein-coupled receptor agonists.  
 XX  
 PS Claim 25; Page 59; 102pp; English.  
 XX  
 CC The present sequence is a cDNA encoding hRUP7, an endogenous human orphan  
 CC G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned  
 CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan  
 CC GPCR of the invention, like all GPCRs has seven transmembrane alpha  
 CC helices with an extracellular N-terminus and an intracellular C-terminus.  
 CC However, no endogenous ligands has yet been identified for the proteins  
 CC of the invention. The orphan GPCRs may be used in the identification of  
 CC their endogenous ligands, and to screen potential GPCR agonists and  
 CC antagonists for use as pharmaceutical agents. The proteins may also be  
 CC used in the study of GPCR-mediated signalling cascades, and to elucidate  
 CC their precise role in normal and diseased human conditions. Nucleic acid  
 CC encoding human orphan GPCRs may be used for tissue localisation in  
 CC expression analysis to provide information about their function in  
 CC healthy and pathological states  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Query Match 1.9%; Score 22; DB 3; Length 1173;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 966 TCTGTTCAAAATGTCCTTTCA 987  
 DB 960 TCTGTTCAAAATGTCCTTTCA 981  
 RESULT 14  
 AAF83203  
 ID AAF83203 standard; cDNA; 1173 BP.  
 XX  
 AC AAF83203;  
 XX  
 DT 09-JUL-2001 (first entry)  
 XX  
 DE Human GPCR-like polypeptide, PFI-013 encoding cDNA.  
 XX  
 KW G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiashtmatic;  
 KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;

KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;  
 KW signal transduction; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..1173  
 FT CDS /\*tag= a  
 FT /product= "PFI-013"  
 XX  
 PN EPI096009-A1.  
 XX  
 PD 02-MAY-2001.  
 XX  
 PF 24-OCT-2000; 2000EP-00309364.  
 XX  
 PR 29-OCT-1999; 99GB-00025641.  
 PR 20-APR-2000; 2000GB-00009973.  
 XX  
 PA (PFI3 ) PFIZER LTD.  
 PA (PFI3 ) PFIZER INC.  
 XX  
 PI Peter B, O'reilly MA;  
 XX  
 DR WPI; 2001-309854/33.  
 DR P-PSDB; AAB62445.  
 XX  
 PT New G-protein coupled receptor-like polypeptide, polynucleotide for  
 PT screening drug candidates for treating diseases associated with signal  
 PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.  
 XX  
 PS Claim 1; Page 43; 66pp; English.  
 XX  
 CC This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor  
 CC (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be  
 CC expressed by standard recombinant methodology. Antibodies and modulators  
 CC of PFI-013 are useful in the manufacture of a medicament for treating  
 CC allergic disorder, including extrinsic asthma, immunological disorders,  
 CC such as intrinsic asthma, vasculitic granulomatous disease, interstitial  
 CC and other pulmonary disease, including chronic obstructive pulmonary  
 CC disease (COPD), infectious, inflammatory disease, such as inflammatory  
 CC bowel disease and neoplastic and myeloproliferative diseases. They are  
 CC also useful for treating obesity, diabetes, metabolic, neurological and sexual  
 CC diseases, psychotherapeutics, urogenital disease, reproduction and sexual  
 CC medicine, inflammation, cancer, tissue repair, dermatology, photocoagling,  
 CC skin pigmentation, osteoporosis, cardiovascular, gastrointestinal  
 CC diseases, allergy and respiratory disease, sensory organ disorders, sleep  
 CC disorders and hair loss. The PFI-013 protein and nucleic acid are useful  
 CC in the diagnosis and treatment of the above conditions and also for  
 CC screening drug candidates for the treatment of diseases associated with  
 CC signal transduction. The antibodies are also useful for enrichment of  
 CC eosinophils from mammalian, especially human blood and for detecting the  
 CC protein in biological samples  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Query Match 1.9%; Score 22; DB 4; Length 1173;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 966 TCTGTTCAAAATGTCCTTTCA 987  
 DB 960 TCTGTTCAAAATGTCCTTTCA 981  
 RESULT 15  
 AAH24007  
 ID AAH24007 standard; cDNA; 1173 BP.  
 XX  
 AC AAH24007;  
 XX  
 DT 10-AUG-2001 (first entry)  
 XX

DE Human G protein-coupled receptor AXOR35 cDNA.

XX AXOR35; human; G protein-coupled receptor; 7TM receptor;

XX histamine H3 receptor homologue; infection; viral; bacterial; fungal;

KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;

KW bulimia; osteoporosis; asthma; allergy; urinary retention;

KW acute heart failure; hypotension; hypertension; angina pectoris;

KW myocardial infarction; stroke; ulcer; migraine; vomiting;

KW psychotic disorder; neurological disorder; depression; anxiety; schizophrenia;

KW manic depression; bipolar disorder; depression; delirium; dementia;

KW severe mental retardation; dyskinesia; Parkinson's disease;

KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;

KW macrophage; eosinophil; neutrophil; function modulation;

KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;

KW drug screening; signal transduction; transgenic animal; drug discovery;

XX ss.

XX Homo sapiens.

XX OS

XX Key Location/Qualifiers

EH 1..1173

FT /\*tag= a

FT /product= "Human AXOR35"

FT /note= "G protein-coupled receptor"

XX W0200133221-AL.

XX 10-MAY-2001.

XX 26-OCT-2000; 2000WO-US029461.

XX 02-NOV-1999; 99US-00431898.

XX 03-FEB-2000; 2000US-00497790.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;

PI Michalovich D, Morrow DM, Zhu Y;

XX WPI; 2001-316464/33.

DR P-PSDB; AAB73622.

XX Novel G-protein coupled receptor polypeptide and polynucleotide for

PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological

PT disorders and for identifying modulators useful for treating asthma.

XX Claim 2; Page 49-50; 54pp; English.

XX The invention relates to the human G protein-coupled receptor AXOR35

CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments

CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative

CC transmembrane domains and is involved in signal transduction. AXOR35 has

CC homology and structural similarity with G protein-coupled receptors such

CC as the human histamine H3 receptor. The invention also relates to

CC expression vectors and host cells comprising AXOR35 DNA, to recombinant

CC and nucleotides may be used to treat a wide variety of disorders

CC including bacterial, fungal, protozoal and viral infections, particularly

CC HIV-1 or HIV-2 infections; pain; cancer; benign prostatic hypertrophy;

CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;

CC urinary retention; acute heart failure; hypotension; hypertension; angina

CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;

CC psychotic and neurological disorders such as anxiety, schizophrenia,

CC manic depression, depression, delirium, dementia, and severe mental

CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's

CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and

CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and

CC antibodies may be used in screening compounds for their ability to

CC modulate AXOR35 activity or expression. Such AXOR35 modulators are

CC particularly useful for treating asthma, and inhibiting or promoting the

CC function of lymphocytes, macrophages, eosinophils or neutrophils in

CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also

CC

CC useful for diagnosing or determining susceptibility of an individual to a

CC disease via the detection of abnormal levels of protein or mRNA, or via

CC the detection of mutations in the corresponding gene. AXOR35 proteins are

CC also useful for inducing an immunological response in a mammal against

CC the above diseases, and for antibody production. AXOR35 nucleotides are

CC also useful as diagnostic reagents, in chromosome localisation and tissue

CC expression studies, and for producing transgenic animals useful in drug

CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35

CC protein or fragments thereof, and are also useful for treating conditions

CC associated with the expression of the AXOR35 protein. The present

CC sequence represents cDNA encoding human AXOR35

XX

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

XX

XX Query Match 1.9%; Score 22; DB 5; Length 1173;

XX Best Local Similarity 100.0%; Pred. No. 2.5;

XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCACAAATTGTCCTTTCA 987

Db 960 TCTGTTCACAAATTGTCCTTTCA 981

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Job time : 862 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 15:51:39 ; Search time 110 Seconds  
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Title: US-10-626-445-5  
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Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*

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- 3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq.\*
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- 5: /cgn2\_6/prodata/2/ina/PCRUS\_COMB.seq.\*
- 6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	1.9	1173	US-09-414-010-1	Sequence 1, Appli
2	22	1.9	1173	US-09-812-216-1	Sequence 1, Appli
3	21	1.8	867	US-08-466-103A-5	Sequence 5, Appli
4	20	1.7	1085	US-08-466-103A-11	Sequence 11, Appli
5	20	1.7	1085	US-09-016-434-1435	Sequence 1435, Ap
6	20	1.7	1149	US-08-466-103A-3	Sequence 3, Appli
7	19	1.6	453	US-09-134-000C-1014	Sequence 1014, Ap
8	19	1.6	5229	US-09-635-872A-16	Sequence 16, Appl
9	19	1.6	5229	US-09-636-077A-16	Sequence 16, Appl
10	19	1.6	5229	US-09-636-060C-16	Sequence 16, Appl
11	19	1.6	5229	US-09-986-552-16	Sequence 16, Appl
12	19	1.6	152331	US-09-128-155-16	Sequence 16, Appl
13	18	1.5	424	US-09-621-976-7975	Sequence 7975, Ap
14	18	1.5	536	US-08-341-568-1	Sequence 1, Appli
15	18	1.5	536	US-08-911-020-1	Sequence 1, Appli
16	18	1.5	2278	US-09-620-312D-1003	Sequence 1003, Ap
17	18	1.5	2278	US-09-148-545-78	Sequence 78, Appl
18	18	1.5	2278	US-09-148-545-131	Sequence 131, Appl
19	18	1.5	152331	US-09-128-155-16	Sequence 16, Appl
20	18	1.5	176373	US-09-128-155-17	Sequence 17, Appl
21	17	1.4	526	US-08-956-171E-516	Sequence 516, App
22	17	1.4	539	US-08-381-114	Sequence 114, App
23	17	1.4	675	US-09-621-976-2461	Sequence 2461, Ap
24	17	1.4	945	US-08-489-039A-2349	Sequence 2349, App
25	17	1.4	1368	US-09-540-236-405	Sequence 405, App
26	17	1.4	1503	US-09-254-465A-5	Sequence 5, Appli
27	17	1.4	1558	US-09-198-603C-24	Sequence 24, Appli

28	17	1.4	1590	4	US-09-369-247-14	Sequence 14, Appli
29	17	1.4	1620	4	US-09-554-080A-1	Sequence 1, Appli
30	17	1.4	1744	4	US-09-484-970B-83	Sequence 83, Appli
31	17	1.4	2088	4	US-09-489-039A-7167	Sequence 7167, Ap
32	17	1.4	2176	4	US-08-956-171E-445	Sequence 445, App
33	17	1.4	2181	4	US-09-254-465A-7	Sequence 7, Appli
34	17	1.4	2181	4	US-09-254-465A-11	Sequence 11, Appli
35	17	1.4	2565	4	US-09-023-655-1052	Sequence 1052, Ap
36	17	1.4	2861	4	US-09-016-434-1103	Sequence 1103, Ap
37	17	1.4	4746	2	US-08-819-288-2	Sequence 2, Appli
38	17	1.4	4746	4	US-09-400-348-2	Sequence 2, Appli
39	17	1.4	4747	1	US-08-261-822A-2	Sequence 2, Appli
40	17	1.4	4747	5	PCT-US95-07744A-2	Sequence 2, Appli
41	17	1.4	6042	1	US-08-261-822A-1	Sequence 1, Appli
42	17	1.4	6042	5	PCT-US95-07744A-1	Sequence 1, Appli
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45	17	1.4	6387	1	US-07-721-775A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-414-010-1  
; Sequence 1, Application US/09414010  
; Patent No. 6204017  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monsma, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414,010  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-414-010-1

Query Match 1.9%; Score 22; DB 3; Length 1173;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 966 TCTGTTCACAATGTGCTTTCA 987  
Db 960 TCTGTTCACAATGTGCTTTCA 981

RESULT 2  
US-09-812-216-1  
; Sequence 1, Application US/09812216  
; Patent No. 6613533  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monsma, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/812,216  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 09/414,010



APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1435:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 9602129  
US-09-016-434-1435

Query Match 1.7%; Score 20; DB 4; Length 1085;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 940 TTGGCATTGTGGGCTCC 959  
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Db 771 TTGGCATTGTGGGCTCC 790

RESULT 6  
US-08-466-103A-3  
Sequence 3, Application US/08466103A  
Patent No. 5856124  
GENERAL INFORMATION:  
APPLICANT: Reppert, Steven M.  
APPLICANT: Ebisawa, Takashi  
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,103A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/319,887  
FILING DATE: 07-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/261,857  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00786/250002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1149 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 49...1146  
OTHER INFORMATION:  
US-08-466-103A-3

Query Match 1.7%; Score 20; DB 2; Length 1149;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 940 TTGGCATTGTGGGCTCC 959  
|||||  
Db 835 TTGGCATTGTGGGCTCC 854

RESULT 7  
US-09-134-000C-1014/c  
Sequence 1014, Application US/09134000C  
Patent No. 6617156  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
PRIOR FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1014  
LENGTH: 453  
TYPE: DNA  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-1014

Query Match 1.6%; Score 19; DB 4; Length 453;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 AATTATTTTCTTAATT 169  
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Db 282 AATTATTTTCTTAATT 264

RESULT 8  
US-09-635-872A-16/c  
Sequence 16, Application US/09635872A  
Patent No. 6534300

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; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 195613US0
; CURRENT APPLICATION NUMBER: US/09/635,872A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 5229
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-635-872A-16

Query Match      1.6%; Score 19; DB 4; Length 5229;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1022 GGTACAGCATTGCCTTCTG 1040
Db      2576 GGTACAGCATTGCCTTCTG 2558

RESULT 9
US-09-636-077A-16/c
; Sequence 16, Application US/09636077A
; Patent No. 6537785
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
; FILE REFERENCE: 195612US0
; CURRENT APPLICATION NUMBER: US/09/636,077A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 5229
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-636-077A-16

Query Match      1.6%; Score 19; DB 4; Length 5229;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1022 GGTACAGCATTGCCTTCTG 1040
Db      2576 GGTACAGCATTGCCTTCTG 2558

RESULT 10
US-09-636-060C-16/c
; Sequence 16, Application US/09636060C
; Patent No. 6642038
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM M
; TITLE OF INVENTION: GLCNAC PHOSPHOTRANSFERASE OF THE LYSOSOMAL TARGETING PATHWAY
; FILE REFERENCE: 210119US0CONT
; CURRENT APPLICATION NUMBER: US/09/636,060C
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 5229
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-636-060C-16
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Query Match      1.6%; Score 19; DB 4; Length 5229;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1022 GGTACAGCATTGCCTTCTG 1040
Db      2576 GGTACAGCATTGCCTTCTG 2558

RESULT 11
US-09-986-552-16/c
; Sequence 16, Application US/09986552
; Patent No. 6670165
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 215089US77DIV
; CURRENT APPLICATION NUMBER: US/09/986,552
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/635,872
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 5229
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-986-552-16

Query Match      1.6%; Score 19; DB 4; Length 5229;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1022 GGTACAGCATTGCCTTCTG 1040
Db      2576 GGTACAGCATTGCCTTCTG 2558

RESULT 12
US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) -- (152331)
; OTHER INFORMATION: n = A,T,C or G
; US-09-128-155-16

Query Match      1.6%; Score 19; DB 3; Length 152331;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      911 CCAGGTACTGGCCATCCT 929
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Db 135343 CCAGGTCACTGGCCATCCT 135325  
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## RESULT 13

US-09-621-976-7975  
; Sequence 7975, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 7975  
; LENGTH: 424  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-7975

Query Match 1.5%; Score 18; DB 4; Length 424;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 544 CTCCTGGAAATTCCTGTT 561

Db 40 CTCCTGGAAATTCCTGTT 57

## RESULT 14

US-08-341-568-1  
; Sequence 1, Application US/08341568  
; Patent No. 5661021  
; GENERAL INFORMATION:  
; APPLICANT: Buchert, Johanna  
; APPLICANT: Siika-aho, Matti  
; APPLICANT: Viikari, Liisa  
; APPLICANT: Penttala, Merja  
; APPLICANT: Saloheimo, Anu  
; APPLICANT: Marjatta, Rannu  
; TITLE OF INVENTION: Mannanase enzymes, genes coding for them.  
; TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching lig  
; TITLE OF INVENTION: pulps  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch and Birch  
; STREET: PO Box 747  
; CITY: Falls Church  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/341,568  
; FILING DATE: 22-NOV-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy Jr, Gerald M  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 365-262P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 536 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Trichoderma reesei  
; STRAIN: QM9414  
US-08-341-568-1

Query Match 1.5%; Score 18; DB 1; Length 536;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 CTGGAGCCTGTGGAAGCG 617

Db 128 CTGGAGCCTGTGGAAGCG 145

## RESULT 15

US-08-911-020-1  
; Sequence 1, Application US/08911020  
; Patent No. 5854047  
; GENERAL INFORMATION:  
; APPLICANT: Buchert, Johanna  
; APPLICANT: Siika-aho, Matti  
; APPLICANT: Viikari, Liisa  
; APPLICANT: Penttala, Merja  
; APPLICANT: Saloheimo, Anu  
; APPLICANT: Marjatta, Rannu  
; TITLE OF INVENTION: Mannanase enzymes, genes coding for them,  
; TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching  
; TITLE OF INVENTION: lignocellulosic pulps  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch and Birch  
; STREET: PO Box 747  
; CITY: Falls Church  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,020  
; FILING DATE: 13-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/341,568  
; FILING DATE: 22-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy Jr, Gerald M  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 365-262P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 536 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Trichoderma reesei  
; STRAIN: QM9414  
US-08-911-020-1

Query Match 1.5%; Score 18; DB 2; Length 536;  
Best Local Similarity 100.0%; Pred.No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 CTGGAGCCTGTGGAGCG 617  
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Db 128 CTGGAGCCTGTGGAGCG 145

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Job time : 113 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 17:38:54 ; Search time 660 Seconds  
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Title: US-10-626-445-5  
Perfect score: 1176  
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Searched: 3340653 seqs, 2534783454 residues

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- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	22	1.9	223	17	US-10-283-975A-697
2	22	1.9	1173	9	US-09-812-216-1
3	22	1.9	1173	9	US-09-910-411-1
4	22	1.9	1173	13	US-10-349-253A-1
5	22	1.9	1173	13	US-09-875-076-13
6	22	1.9	1173	13	US-09-876-252-13
7	22	1.9	1173	14	US-10-052-193-1
8	22	1.9	1173	15	US-10-230-078-26
9	22	1.9	1173	15	US-10-272-983-13
10	22	1.9	1173	15	US-10-354-769-1
11	22	1.9	1173	15	US-10-333-807-13
12	22	1.9	1173	16	US-10-417-820A-13
13	22	1.9	1173	17	US-10-723-955-13
14	22	1.9	1173	17	US-10-737-619-1

15	22	1.9	1173	17	US-10-782-596-13	Sequence 13, Appl
16	22	1.9	1265	15	US-10-290-078-25	Sequence 25, Appl
17	22	1.9	1266	10	US-09-891-138A-5	Sequence 5, Appl
18	22	1.9	1300	10	US-09-852-165-1	Sequence 1, Appl
19	22	1.9	1300	17	US-10-696-673-1	Sequence 1, Appl
20	22	1.9	3689	15	US-10-225-567A-628	Sequence 628, App
21	21	1.8	633	13	US-10-027-632-274218	Sequence 274218, App
22	21	1.8	633	16	US-10-027-632-274218	Sequence 274218, App
23	21	1.8	76410	13	US-10-087-192-70	Sequence 70, Appl
24	21	1.8	220895	17	US-10-775-169-88	Sequence 88, Appl
25	21	1.7	248	15	US-10-029-386-25558	Sequence 25558, A
26	20	1.7	536	10	US-09-791-279-37	Sequence 37, Appl
27	20	1.7	543	15	US-10-029-386-11858	Sequence 11858, A
28	20	1.7	1053	15	US-10-112-356-6	Sequence 6, Appl
29	20	1.7	1085	16	US-10-305-720-1435	Sequence 1435, Ap
30	20	1.7	1326	17	US-10-398-036-19	Sequence 19, Appl
31	20	1.7	1552	13	US-10-027-632-263186	Sequence 263186, App
32	20	1.7	1552	16	US-10-027-632-263186	Sequence 263186, App
33	20	1.7	2049	15	US-10-225-567A-163	Sequence 163, App
34	20	1.7	2897	13	US-10-027-632-252125	Sequence 252125, App
35	20	1.7	2897	16	US-10-027-632-252125	Sequence 252125, App
36	19	1.6	355	10	US-09-814-353-5355	Sequence 5355, Ap
37	19	1.6	355	10	US-09-814-353-11642	Sequence 11642, A
38	19	1.6	415	10	US-09-814-353-18026	Sequence 18026, A
39	19	1.6	487	13	US-10-027-632-88455	Sequence 88455, A
40	19	1.6	487	13	US-10-027-632-307248	Sequence 307248, App
41	19	1.6	487	16	US-10-027-632-88455	Sequence 88455, A
42	19	1.6	487	16	US-10-027-632-307248	Sequence 307248, App
43	19	1.6	500	10	US-09-918-995-37950	Sequence 37950, A
44	19	1.6	531	9	US-09-893-737-21	Sequence 21, Appl
45	19	1.6	566	13	US-10-027-632-207090	Sequence 207090, App

ALIGNMENTS

RESULT 1

US-10-283-975A-697  
; Sequence 697, Application US/10283975A  
; Publication No. US20040110792A1  
; GENERAL INFORMATION:  
; APPLICANT: Ortho-Clinical Diagnostics, Inc.  
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia  
; FILE REFERENCE: CDS 293 PCT  
; CURRENT APPLICATION NUMBER: US/10/283,975A  
; PRIOR FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: 60/340,938  
; PRIOR FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 60/338,997  
; PRIOR FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 60/340,081  
; PRIOR FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 60/341,012  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 900  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 697  
; LENGTH: 223  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(223)  
; OTHER INFORMATION: N=any base  
US-10-283-975A-697

Query Match 1.9%; Score 22; DB 17; Length 223;  
Best Local Similarity 100.0%; Pred. No. 0.87;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCCACATTGCTCTTCA 987  
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Db 197 TCTGTTCCACATTGCTCTTCA 218  
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RESULT 2
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas W.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

Query Match          1.9%; Score 22; DB 9; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCAACAATTGCTCTTCA 987
Db 960 TCTGTTCAACAATTGCTCTTCA 981

RESULT 3
US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Query Match          1.9%; Score 22; DB 9; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCAACAATTGCTCTTCA 987
Db 960 TCTGTTCAACAATTGCTCTTCA 981

RESULT 4
US-10-349-253A-1
; Sequence 1, Application US/10349253A
; Publication No. US20040043393A1
; GENERAL INFORMATION:
; APPLICANT: Aubart, Kelly
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Graybill, Todd
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Morrow, Dwight
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C2
; CURRENT APPLICATION NUMBER: US/10/349,253A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/910,411
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-349-253A-1

Query Match          1.9%; Score 22; DB 13; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCAACAATTGCTCTTCA 987
Db 960 TCTGTTCAACAATTGCTCTTCA 981

RESULT 5
US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
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/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,127
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/ PRIOR APPLICATION NUMBER: 60/137,131
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/141,448
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 60/156,653
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,633
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,555
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,634
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/157,280
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,294
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,281
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,293
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,282
/ PRIOR FILING DATE: 1999-10-01
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-875-076-13
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Query Match
Best Local Similarity 100.0%; Score 22; DB 13; Length 1173;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 966 TCTGTTCAAAATGTCCTTTCA 987
Db 960 TCTGTTCAAAATGTCCTTTCA 981
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RESULT 6
US-09-876-252-13
/ Sequence 13, Application US/09876252
/ Publication No. US20030018182A1
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Lehmann-Bruinsma, Karin
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Lin, I-Lin
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Chen, Kuoping
/ APPLICANT: Liaw, Chen W.
/ TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Rec
/ FILE REFERENCE: ARN-0054
/ CURRENT APPLICATION NUMBER: US/09/876,252
/ CURRENT FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 09/416,760
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/110,060
/ PRIOR FILING DATE: 1998-11-27
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,852
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/123,944
/ PRIOR FILING DATE: 1999-03-12
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/ PRIOR APPLICATION NUMBER: 60/123,945
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,951
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/152,524
/ PRIOR FILING DATE: 1999-09-03
/ PRIOR APPLICATION NUMBER: 60/151,114
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: 60/108,029
/ PRIOR FILING DATE: 1998-11-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,127
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,131
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/141,448
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/156,555
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/157,280
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,294
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,281
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,282
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/156,633
/ PRIOR FILING DATE: 1999-09-29
/ NUMBER OF SEQ ID NOS: 146
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-876-252-13
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Query Match
Best Local Similarity 100.0%; Score 22; DB 13; Length 1173;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 966 TCTGTTCAAAATGTCCTTTCA 987
Db 960 TCTGTTCAAAATGTCCTTTCA 981
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RESULT 7
US-10-052-193-1
/ Sequence 1, Application US/10052193
/ Publication No. US20020132755A1
/ GENERAL INFORMATION:
/ APPLICANT: Pfizer, Inc.
/ TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
/ FILE REFERENCE: PCI0963A
/ CURRENT APPLICATION NUMBER: US/10/052,193
/ CURRENT FILING DATE: 2002-01-17
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; PRIOR APPLICATION NUMBER: 0101223.6  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-052-193-1

Query Match 1.9%; Score 22; DB 14; Length 1173;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCAACAATTGTCCTTTCA 987  
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Db 960 TCTGTTCAACAATTGTCCTTTCA 981

## RESULT 8

US-10-290-078-26  
; Sequence 26, Application US/102900078  
; Publication No. US20030124596A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph A.  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692 or 58874  
; FILE REFERENCE: MP12001-288P1(M)  
; CURRENT APPLICATION NUMBER: US/10/290,078  
; CURRENT FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1173)  
US-10-290-078-26

Query Match 1.9%; Score 22; DB 15; Length 1173;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCAACAATTGTCCTTTCA 987  
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Db 960 TCTGTTCAACAATTGTCCTTTCA 981

## RESULT 9

US-10-272-983-13  
; Sequence 13, Application US/10272983  
; Publication No. US20030148450A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/272,983  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946

; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-272-983-13

Query Match 1.9%; Score 22; DB 15; Length 1173;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCAACAATTGTCCTTTCA 987  
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Db 960 TCTGTTCAACAATTGTCCTTTCA 981

## RESULT 10

US-10-354-769-1  
; Sequence 1, Application US/10354769  
; Publication No. US20030149242A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: O'Reilly, Mark A.  
; APPLICANT: Peter, Beate  
; TITLE OF INVENTION: NOVEL POLYPEPTIDE  
; FILE REFERENCE: PC10373B  
; CURRENT APPLICATION NUMBER: US/10/354,769  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US 09/698,801  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/211,243  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: GB 9925641.4  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: GB 0009973.9  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-354-769-1

Query Match 1.9%; Score 22; DB 15; Length 1173;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 966 TCTGTTCAACAATTGTCCTTTCA 987  
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Db 960 TCTGTTCAACAATTGTCCTTTCA 981

## RESULT 11

US-10-393-807-13  
; Sequence 13, Application US/10393807  
; Publication No. US20030175891A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.

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; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-393-807-13

Query Match      1.9%; Score 22; DB 15; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTCAAAATGTCCTTTCA 987
Db 960 TCTGTTCAAAATGTCCTTTCA 981

RESULT 12
US-10-417-820A-13
; Sequence 13, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1999-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-820A-13
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-820A-13

Query Match      1.9%; Score 22; DB 16; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 960 TCTGTTCAAAATGTCCTTTCA 981

RESULT 13
US-10-723-955-13
; Sequence 13, Application US/10723955
; Publication No. US20040110238A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lin, I-Lin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lehman-Bruinsma, Karin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Gore, Martin
; APPLICANT: White, Carol
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; FILE REFERENCE: 7.US29.CON
; CURRENT APPLICATION NUMBER: US/10/723,955
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 10/417,820
; PRIOR FILING DATE: 2003-4-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-955-13
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Query Match 1.9%; Score 22; DB 17; Length 1173;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTTCAACAATTGTCCTTTCA 987  
Db 960 TCTGTTTCAACAATTGTCCTTTCA 981

## RESULT 14

US-10-737-619-1  
; Sequence 1, Application US/10737619  
; Publication No. US20040138234A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer, Inc.  
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS  
; FILE REFERENCE: FC10963A  
; CURRENT APPLICATION NUMBER: US/10/737,619  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: 0101223.6  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-737-619-1

Query Match 1.9%; Score 22; DB 17; Length 1173;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTTCAACAATTGTCCTTTCA 987  
Db 960 TCTGTTTCAACAATTGTCCTTTCA 981

## RESULT 15

US-10-782-596-13  
; Sequence 13, Application US/10782596  
; Publication No. US20040137509A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/782,596  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US/09/875,076  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-782-596-13

Query Match 1.9%; Score 22; DB 17; Length 1173;  
Best Local Similarity 100.0%; Pred. No. 0.93;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 TCTGTTTCAACAATTGTCCTTTCA 987  
Db 960 TCTGTTTCAACAATTGTCCTTTCA 981

Search completed: October 1, 2004, 20:18:26  
Job time : 664 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 14:37:09 ; Search time 3518 seconds

(without alignments)

9982.355 Million cell updates/sec

Title: US-10-626-445-5

Perfect score: 1176

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Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_htc.\*

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19: em\_gss\_pln.\*

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22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C	5	21	1.8	331	29	CE700949
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C	7	21	1.8	722	28	CE849215
	8	21	1.8	861	28	BZ227627
	9	21	1.8	869	29	AY405330
	10	21	1.8	869	29	AY405331
	11	21	1.8	1023	12	BG563625
	12	21	1.8	1103	14	CF661120
	13	20	1.7	251	9	AZ50969
	14	20	1.7	271	28	AZ491769
	15	20	1.7	279	14	CB981626
	16	20	1.7	360	14	D70276
	17	20	1.7	360	14	D70608
	18	20	1.7	373	13	C69245
	19	20	1.7	418	28	CE642921
	20	20	1.7	465	28	AZ150613
	21	20	1.7	485	28	AQ181200
	22	20	1.7	525	9	AL375854
	23	20	1.7	528	29	CE738419
	24	20	1.7	537	28	BH501816
	25	20	1.7	539	12	BG906643
	26	20	1.7	547	28	BZ473862
	27	20	1.7	550	10	BF056033
	28	20	1.7	567	28	AZ250002
	29	20	1.7	575	12	BJ152289
	30	20	1.7	592	28	BH289608
	31	20	1.7	617	28	AZ559416
	32	20	1.7	623	14	CB348956
	33	20	1.7	632	14	CB349043
	34	20	1.7	636	9	AU217737
	35	20	1.7	636	29	CG960774
	36	20	1.7	650	28	AZ471542
	37	20	1.7	654	14	CB914678
	38	20	1.7	660	28	BZ050817
	39	20	1.7	676	28	BZ392492
	40	20	1.7	684	28	BH987629
	41	20	1.7	686	29	CG752731
	42	20	1.7	687	14	CF538979
	43	20	1.7	697	28	AZ381267
	44	20	1.7	699	14	CA375189
	45	20	1.7	704	14	CF147821

#### ALIGNMENTS

RESULT 1  
CG392906  
LOCUS  
DEFINITION  
ZMMBc0004Allf ZMMBc (EcoRI) Zea mays subsp. mays genomic clone  
ZMMBc0004All 5', genomic survey sequence.  
ACCESSION  
CG392906  
VERSION  
CG392906.1 GI:34336131  
KEYWORDS  
GSS.  
SOURCE  
Zea mays subsp. mays (maize)  
ORGANISM  
Zea mays subsp. mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
1 (bases 1 to 997)  
AUTHORS  
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,  
Rouzaud,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.  
TITLE  
Sequencing of the maize genome at PGR (2003b)  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Bharti,A.K.  
Dr.Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: T7

Class: BAC ends  
High quality sequence start: 97.  
FEATURES  
source  
1. .997  
Location/Qualifiers

/organism="Zea mays subsp. mays"  
/mol\_type="genomic DNA"  
/submitter="B73"  
/sub\_species="mays"  
/db\_xref="taxon:4578"  
/clone="ZMMBCC0004A11"  
/lab\_host="E. coli DH10B"  
/clone\_lib="ZMMBCC (ECORI)"  
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI"

## ORIGIN

Query Match 2.0%; Score 23; DB 29; Length 997;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 57 ATTTTAAATGCTTCATTGGCT 79  
|||||  
Db 402 ATTTTAAATGCTTCATTGGCT 424  
|||||

RESULT 2  
CC226484/c  
LOCUS  
DEFINITION  
CH261-69015\_RM1.1 CH261 Gallus gallus genomic clone CH261-69015,  
genomic survey sequence.  
GSS.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Gallus gallus (chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

REFERENCE  
AUTHORS  
Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,  
Warren, W., Graves, T., Mardis, E. and Wilson, R.  
Gallus gallus BAC End Reads  
Unpublished (2003)

TITLE  
JOURNAL  
COMMENT  
Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@wustl.edu  
Insert Length: 182000 Std Error: 0.00  
Seq primer: RM1 TAGACTCTACTATAGGAGA  
Class: BAC ends  
High quality sequence start: 19  
High quality sequence stop: 360.

FEATURES  
source  
1. .1051  
Location/Qualifiers

/organism="Gallus gallus"  
/mol\_type="genomic DNA"  
/strain="Red Jungle Fowl"  
/db\_xref="taxon:9031"  
/clone="CH261-69015"  
/sex="female"  
/cell\_line="UCD001, inbred 256"  
/clone\_lib="CH261"  
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;  
CH261 Female Chicken library - for library and clone  
ordering information: http://www.chori.org/bacpac"

## ORIGIN

Query Match 2.0%; Score 23; DB 28; Length 1051;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 151 AATTATTTTCTTAAATTTGGC 173  
|||||  
Db 849 AATTATTTTCTTAAATTTGGC 827  
|||||

RESULT 3  
BB418962  
LOCUS  
DEFINITION

BB418962 RIKEN full-length enriched, 12 days embryo spinal cord Mus  
musculus cDNA clone C530014D15 3' similar to APl17947 Homo sapiens  
P2Z domain-containing guanine nucleotide exchange factor I mRNA,  
mRNA sequence.  
BB418962  
VERSION  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
1 (bases 1 to 274)  
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,  
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,  
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,  
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,  
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,  
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,  
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,  
Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Sugahara, Y., Suzuki, H., Tsunoda, Y., Watanabe, A.,  
Takahashi, F., Tominaga, N., Toyota, T., Tsunoda, Y., Watanabe, A.,  
Watanabe, S., Yamamura, T., Yamashita, I., Yano, R., Yasunishi, A.,  
Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and  
Hayashizaki, Y.

REFERENCE  
AUTHORS

RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,  
Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermotabilization and thermostabilization of thermolabile enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Katsunai, T., Akiyama, J., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
Tomaru, Y., Carninci, P., Shibata, Y., Okazaki, Y., and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)

TITLE  
JOURNAL  
COMMENT

RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,  
Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermotabilization and thermostabilization of thermolabile enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Katsunai, T., Akiyama, J., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
Tomaru, Y., Carninci, P., Shibata, Y., Okazaki, Y., and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.  
Location/Qualifiers  
1. .274  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="C530014D15"  
/tissue\_type="spinal cord"  
/dev\_stage="12 days embryo"  
/lab\_host="DH10B"  
/clone\_lib="RIKEN full-length enriched, 12 days embryo  
spinal cord"

/note="Site 1: Sali; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was

FEATURES  
source  
1. .274  
Location/Qualifiers

/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="C530014D15"  
/tissue\_type="spinal cord"  
/dev\_stage="12 days embryo"  
/lab\_host="DH10B"  
/clone\_lib="RIKEN full-length enriched, 12 days embryo  
spinal cord"  
/note="Site 1: Sali; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was



**AUTHORS** Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.  
**TITLE** Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

**JOURNAL COMMENT** Unpublished (1997)  
 Other GSSs: CITBI-El-2544B13.TF  
 Contact: Shaying Zhao, William Nierman, Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: hbe@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page:  
[http://www.tigr.org/tcdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html).  
 Seq primer: M13 Reverse  
 Class: BAC ends.

**FEATURES** source  
 1..602  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="2544B13"  
 /sex="male"  
 /cell\_type="sperm"  
 /clone\_lib="CITBI-El"  
 /notes="Vector: pBelobAC11; Site\_1: EcoRI; Site\_2: EcoRI;  
 CalTech Human BAC Library D"

**ORIGIN**

Query Match 1.8%; Score 21; DB 28; Length 602;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 640 AGCCATGCTGGATTCTCCACT 660  
 Db 498 AGCCATGCTGGATTCTCCACT 478

**RESULT 7**  
**CE849215/c**  
**LOCUS** tigr-gss-dog-1700032984147 Dog Library Canis familiaris genomic,  
**DEFINITION** genomic survey sequence.

**ACCESSION** CE849215  
**VERSION** CE849215.1 GI:37214951  
**KEYWORDS** GSS.  
**SOURCE** Canis familiaris (dog)  
**ORGANISM** Canis familiaris

**REFERENCE** 1 (bases 1 to 722)  
**AUTHORS** Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Kirksness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.

**TITLE** The dog genome: survey sequencing and comparative analysis

**JOURNAL** Science 301 (5641), 1898-1903 (2003)  
**MEDLINE** 22875432  
**PUBMED** 14512627

**COMMENT** Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

**FEATURES** source  
 1..722  
 Location/Qualifiers  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Foodle"

**ORIGIN**

Query Match 1.8%; Score 21; DB 29; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 GAAGTAATATTTTCTTGA 166  
 Db 188 GAAGTAATATTTTCTTGA 168

**RESULT 8**

BZ227627  
**LOCUS** BZ227627  
**DEFINITION** CH230-400N17.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone  
 CH230-400N17, genomic survey sequence.

**ACCESSION** BZ227627  
**VERSION** BZ227627.1 GI:23886168  
**KEYWORDS** GSS.  
**SOURCE** Rattus norvegicus (Norway rat)  
**ORGANISM** Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

**REFERENCE** 1 (bases 1 to 861)  
**AUTHORS** Zhao,S., Shetty,J., Shatsman,S., Teegaye,G., Geer,K.,  
 Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,  
 Riggs,F., de Jong,P. and Fraser,C.M.

**TITLE** Rat BAC End Sequences from Library CHORI-230 MboI segment  
**JOURNAL** Unpublished (1999)  
**COMMENT** Other GSSs: CH230-400N17.TJ  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230  
 (http://www.chori.org/bacpac/rat230.htm). For BAC library  
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/or ering\_information.htm). BAC end  
 plate: http://www.tigr.org/tadb/bac\_ends/rat/bac\_end\_intro.html  
 Seq primer: T7  
 Class: BAC ends.

**FEATURES**

source  
 1..861  
 Location/Qualifiers  
 /organism="Rattus norvegicus"  
 /mol\_type="genomic DNA"  
 /strain="BN/SsNHsd/MCW"  
 /db\_xref="taxon:10116"  
 /clone="CH230-400N17"  
 /sex="Female"  
 /cell\_type="Brain"  
 /clone\_lib="CHORI-230 Segment 2"  
 /notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by  
 Pieter de Jong"

**ORIGIN**

Query Match 1.8%; Score 21; DB 28; Length 861;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TTGTATTTCCATTCCTCTGTA 215  
 Db 452 TTGTATTTCCATTCCTCTGTA 472

/db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /notes="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"



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RESULT 9
AY405330
LOCUS
DEFINITION Homo sapiens MTNR1A gene, GSS 16-DEC-2003
ACCESSION AY405330
VERSION AY405330.1 GI:39761304
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 869)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
2 (bases 1 to 869)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment
FEATURES
source
Location/Qualifiers
1..869
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>869
/gene="MTNR1A"
/locus_tag="HCM2188"

gene

ORIGIN
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Best Local Similarity 100.0%; Pred.No. 34;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 939 TTTTCCCATTTGCTGGGCTCC 959
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Db 554 TTTTCCCATTTGCTGGGCTCC 574

RESULT 10
AY405331
LOCUS
DEFINITION Pan troglodytes MTNR1A gene, GSS 16-DEC-2003
ACCESSION AY405331
VERSION AY405331.1 GI:39761305
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 (bases 1 to 869)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302

```

```

REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment
FEATURES
source
Location/Qualifiers
1..869
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>869
/gene="MTNR1A"
/locus_tag="HCM2188"

gene

ORIGIN
Query Match 1..869 Score 21; DB 29; Length 869;
Best Local Similarity 100.0%; Pred.No. 34;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 939 TTTTCCCATTTGCTGGGCTCC 959
|||||
Db 554 TTTTCCCATTTGCTGGGCTCC 574

RESULT 11
BG563625/c
LOCUS
DEFINITION BG563625.1 GI:13571277
ACCESSION BG563625
VERSION BG563625
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1023)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1548 row: k column: 18
High quality sequence stop: 502.
FEATURES
Location/Qualifiers
1..1023
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4710281"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_76"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site: 1:
SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,

```

CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 1.8%; Score 21; DB 12; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 150 TAATATTATTTTCTTAATTT 170  
|||||  
Db 720 TAATATTATTTTCTTAATTT 700  
|||||

## RESULT 12

CF6611120 1103 bp mRNA linear EST 07-OCT-2003  
LOCUS CcLL10a33n22f1 Carp liver library 5 Cyprinus carpio cDNA clone  
DEFINITION 33n22 5', mRNA sequence.

ACCESSION CF6611120

VERSION CF6611120.1 GI:37558249

KEYWORDS EST.

SOURCE Cyprinus carpio (common carp)

## ORGANISM

Cyprinus carpio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Cyprinus.

## REFERENCE

1 (bases 1 to 1103)  
Gracey, A.Y., Fraser, E., Li, W. and Cossins, A.R.

AUTHORS Microarray and EST analysis of the carp (Cyprinus carpio)

TITLE transcriptome during environmental stress

## JOURNAL

Unpublished (2003)

## COMMENT

Contact: Andrew R. Cossins  
Laboratory for Environmental Gene Regulation  
University of Liverpool  
School of Biological Sciences, The Biosciences Building, Crown  
Street, Liverpool, United Kingdom, L69 7ZB  
Tel: +44 (0)151-795-4510  
Fax: +44 (0)151-795-4431  
Email: cossins@liv.ac.uk  
Vector has been trimmed from this EST.  
Plate: 33 row: n column: 22  
Seq primer: Triplex 5' LD (5'-CTCGGAGCGGCCATCTGTGTGT-3')  
High quality sequence start: 35  
High quality sequence stop: 830.

## FEATURES

source

1..1103  
Location/Qualifiers  
/organism="Cyprinus carpio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7962"  
/clone="33n22"  
/sex="Male & female"  
/tissue\_type="Liver"  
/dev\_stage="Adult"  
/lab\_host="E.coli Electronax DH10B"  
/clone\_lib="Carp liver library 5"  
/notes="Vector: pTriplex2; Site 1: SfiI GGCCATTAGCGCC;  
Site 2: SfiI GGCGCTCGGCC; Serially subtracted cDNA  
library prepared from liver of warm, cold and hypoxia  
challenged animals"

## ORIGIN

Query Match 1.8%; Score 21; DB 14; Length 1103;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

540 AATGCTCTTGGAAATCTCTGCT 560  
|||||

## Db

214 AATGCTCTTGGAAATCTCTGCT 234  
|||||

## RESULT 13

AA250969 251 bp mRNA linear EST 13-AUG-1997  
LOCUS z507a11.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:684524 3'  
DEFINITION

similar to contains Alu repetitive element;; mRNA sequence.

## ACCESSION

AA250969 1 GI:1885930

## VERSION

AA250969.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 251)

## AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

## JOURNAL

Tumor Gene Index

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Seq primer: -41m13 fwd. ET from Amersham

High quality sequence stop: 245.

## FEATURES

source

1..251  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:684524"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GCB1"  
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD-),  
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer  
[5'-TGTTCCAAATCTGAAGTGGAGCGCGCTCATTTTTTTTTTTT-3'  
]. Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Donaldo."

## ORIGIN

Query Match 1.7%; Score 20; DB 9; Length 251;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

910 GCCAGGTCACTGGCCATCCT 929  
|||||

## Db

173 GCCAGGTCACTGGCCATCCT 192  
|||||

## RESULT 14

AZ491769/c

LOCUS

DEFINITION

1M0325H05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0325H05 R, genomic survey sequence.

ACCESSION AZ491769

VERSION AZ491769.1 GI:10663795

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 271)

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D. Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0325 row: H column: 05  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 271.

Location/Qualifiers  
1. 271  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0325H05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gl|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# FEATURES

source

## FEATURES

source

UC Davis, Plant Pathology  
One Shields Ave, Davis, CA 95616, USA  
Tel: 530 754 6561  
Fax: 530 754 6617  
Email: drcook@ucdavis.edu  
Seq primer: ACGGTACCGACATATGCC.  
Location/Qualifiers  
1. 279  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="CAB70005.IIIaF\_B07"  
/sex="Hermaphrodite"  
/dev\_stage="Post-Veraison, 18-19 brix"  
/lab\_host="DH5alpha"  
/clone\_lib="Cabernet Sauvignon Berry Post-Veraison - CAB7"  
/note="Organ: Berry; Vector: pDNR; Site 1: Sfil; Site 2: Sfil; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8 berries. Samples were collected post-veraison from field-grown vines during stage III of berry growth at 89 days after full bloom. Berries soluble solid concentration ranged between 18-19 brix. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directly cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AAGCAGTGGTATCAGCAGAGTGGCATTACGGCGGG-3' and 5'-ATTCTAGAGCGCGCGGACATG-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

## ORIGIN

Query Match 1.7%; Score 20; DB 14; Length 279;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 822 TGCCTTCAAAGTGGGTTCT 841  
|||||  
Db 61 TGCCTTCAAAGTGGGTTCT 42  
|||||

Search completed: October 1, 2004, 18:37:41  
Job time : 3527 secs

Query Match 1.7%; Score 20; DB 28; Length 271;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 TTGATTCCATCTCTGT 214  
|||||  
Db 127 TTGATTCCATCTCTGT 108  
|||||

RESULT 15  
CB981626/c  
LOCUS CB981626 279 bp mRNA linear EST 01-MAY-2003  
DEFINITION CAB70005.IIIaF\_B07 Cabernet Sauvignon Berry Post-Veraison - CAB7  
Vitis vinifera cDNA clone CAB70005.IIIaF\_B07 5', mRNA sequence.  
ACCESSION CB981626  
VERSION CB981626.1 GI:30304832  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.  
REFERENCE 1 (bases 1 to 279)  
AUTHORS Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Jones, K. and Cook, D.  
Expressed sequence tags from cabernet sauvignon berries at various developmental stages  
JOURNAL Unpublished (2003)  
COMMENT Contact: Douglas Cook, PhD  
CAES Genome Facility

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2035	99.4	391	5	AAm50565	Aam50565 Mouse hist
2	1745	85.2	391	5	AAm50566	Aam50566 Rat hist
3	1370.5	66.9	390	3	AAb02831	Aab02831 Human G p
4	1370.5	66.9	390	3	AAy71297	Aay71297 Human exp
5	1370.5	66.9	390	4	AAb62445	Aab62445 Human GPC
6	1370.5	66.9	390	4	AAg64477	Ag64477 Human G p
7	1370.5	66.9	390	4	AAb73622	Aab73622 Human G p
8	1370.5	66.9	390	5	AAm53050	Aam53050 Human G p
9	1370.5	66.9	390	5	ABp98629	Abp98629 Human hist
10	1370.5	66.9	390	5	ABb78276	Abb78276 Amino aci
11	1370.5	66.9	390	5	AAm50564	Aam50564 Human hist
12	1370.5	66.9	390	5	AAg66023	Ag66023 Human hist
13	1370.5	66.9	390	5	AAu74906	Aau74906 Amino aci
14	1370.5	66.9	390	6	ABg71960	Abg71960 Human G-p
15	1370.5	66.9	390	6	ABu92265	Abu92265 Human G p
16	1370.5	66.9	390	6	ABp81727	Abp81727 Human hist
17	1370.5	66.9	390	6	AAe36417	Aae36417 Human H4
18	1370.5	66.9	391	5	AAm53052	Aam53052 Human G p
19	1370.5	66.9	392	5	AAm53053	Aam53053 Human G p
20	1366.5	66.7	390	4	AAm51410	Aam51410 Human GPC
21	1366.5	66.7	390	6	AAE36416	Aae36416 Human H4
22	1238	60.4	389	5	AAm50567	Aam50567 Guinea pi
23	1198	58.5	357	6	AAe36415	Aae36415 Human H4
24	1074.5	52.5	336	6	AAe36414	Aae36414 Human H4
25	729.5	35.6	415	7	AAO29530	Aao29530 Human H3

CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
CC the neuroendocrine system, stress and spasticity  
XX  
SQ Sequence 391 AA;  
  
Query Match 99.4%; Score 2035; DB 5; Length 391;  
Best Local Similarity 99.7%; Pred. No. 1.9e-202;  
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 MSESNSGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDNLRHRSNYFFNLAI 60  
Db 1 MSESNSGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDNLRHRSNYFFNLAI 60  
  
Qy 61 DFLVGLISIPLYIPHLVFNMFNGSGICMFMLITDYLCTASVYVILISYDRYQSVNAV 120  
Db 61 DFLVGLISIPLYIPHLVFNMFNGSGICMFMLITDYLCTASVYVILISYDRYQSVNAV 120  
  
Qy 121 SYRAQHTGIMKIVAQVAVVILAFVNGPMLASDSWKNSNTKDCPFGFVTEWYILIT 180  
Db 121 SYRAQHTGIMKIVAQVAVVILAFVNGPMLASDSWKNSNTKDCPFGFVTEWYILIT 180  
  
Qy 181 MLEFLPLVIVSVAYFNVQIYWSLWKRRALSRCPHAGSTSSASGHLHAGVACRTSN 240  
Db 181 MLEFLPLVIVSVAYFNVQIYWSLWKRRALSRCPHAGSTSSASGHLHAGVACRTSN 240  
  
Qy 241 PGLKESAAHRSHPRRKSSILVSLRTHMNSSITAFKVGSPWRSSEAAALRQREYAEILRG 300  
Db 241 PGLKESAAHRSHPRRKSSILVSLRTHMNSSITAFKVGSPWRSSEAAALRQREYAEILRG 300  
  
Qy 301 RKLARSLAILLSAFALCWAPYCLFTVILSTYPTERPKSVWYSIAFWLQWNSFVNPFY 360  
Db 301 RKLARSLAILLSAFALCWAPYCLFTVILSTYPTERPKSVWYSIAFWLQWNSFVNPFY 360  
  
Qy 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391  
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391  
  
RESULT 2  
AAM50566  
ID AAM50566 standard; protein; 391 AA.  
XX AC AAM50566;  
DT 18-MAR-2002 (first entry)  
DE Rat histamine H4 receptor.  
XX Histamine H4 receptor; rat; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy.  
XX Rattus rattus.  
OS  
XX WO200192485-A1.  
XX PD 06-DEC-2001.  
XX 22-FEB-2001; 2001WO-US005914.  
XX 31-MAY-2000; 2000US-0208260P.  
XX (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX Lovenberg T, Liu C;  
XX WPI; 2002-114339/15.  
XX DR N-PSDB; AAI70982.  
XX  
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
the proteins, useful in gene therapy for treating diseases where it is

PT beneficial to elevate mammalian histamine H4 receptor activity.

XX Claim 13; Fig 6A; 92pp; English.

XX The present sequence is that of a rat histamine receptor of the H4  
CC subtype, as predicted from a cDNA clone isolated from a spleen cDNA  
CC library. The invention provides mammalian (human, mouse, rat and guinea  
CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
CC recombinant host cells that produce active recombinant protein. The  
CC pharmacology of known histamine ligands is demonstrated. Mammalian  
CC histamine H4 receptor may be used in gene therapy for the treatment of  
CC diseases where it is beneficial to elevate mammalian histamine H4  
CC receptor activity. Recombinant protein is useful for identifying  
CC modulators of the histamine H4 receptor. Such modulators may be useful  
CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
CC the neuroendocrine system, stress and spasticity  
XX

SQ Sequence 391 AA;

Query Match 85.2%; Score 1745; DB 5; Length 391;

Best Local Similarity 84.9%; Pred. No. 2.6e-172; Indels 0; Gaps 0;  
Matches 332; Conservative 17; Mismatches 42;

Qy 1 MSESNSGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDNLRHRSNYFFNLAI 60  
Db 1 MSESNGTDVPLTAQVPLAFMSSLAFAITIGNAVVILAFVADNLRHRSNYFFNLAI 60  
  
Qy 61 DFLVGLISIPLYIPHLVFNMFNGSGICMFMLITDYLCTASVYVILISYDRYQSVNAV 120  
Db 61 DFPVGVISIPLYIPHTLFNMFNGSGICMFMLITDYLCTASVYVILISYDRYQSVNAV 120  
  
Qy 121 SYRAQHTGIMKIVAQVAVVILAFVNGPMLASDSWKNSNTKDCPFGFVTEWYILIT 180  
Db 121 RYRAQHTGILKIVAQVAVVILAFVNGPMLASDSWKNSNTBECEFGFVTEWYILIT 180  
  
Qy 181 MLEFLPLVIVSVAYFNVQIYWSLWKRRALSRCPHAGSTSSASGHLHAGVACRTSN 240  
Db 181 AFLEFLPLVIVSVQIYWSLWKRGSLRCPHAGFIATSSRGTGHSRRRTGLACRTSL 240  
  
Qy 241 PGLKESAAHRSHPRRKSSILVSLRTHMNSSITAFKVGSPWRSSEAAALRQREYAEILRG 300  
Db 241 PGLKEPAASHSESHPRGKSSLLVSLRTHMSSGIIAFKVGSPCRSESPVLHQREHVELL 300  
  
Qy 301 RKLARSLAILLSAFALCWAPYCLFTVILSTYPTERPKSVWYSIAFWLQWNSFVNPFY 360  
Db 301 RKLARSLAVLLSFAFALCWAPYCLFTVILSTYPTERPKSVWYSIAFWLQWNSLINFY 360  
  
Qy 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391  
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391

RESULT 3

AAB02831

ID AAB02831 standard; protein; 390 AA.

XX AC AAB02831;

XX 22-AUG-2000 (first entry)

XX Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.

XX Human; G protein coupled receptor; GPCR; transmembrane receptor;  
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant.

XX Homo sapiens.

XX WO200022131-A2.

XX 20-APR-2000.



PT Novel human orphan G protein-coupled receptors and the encoding cDNAs for  
PT use in the identification of G protein-coupled receptor agonists.  
XX  
PS Claim 26; Page 60-61; 102pp; English.

XX The present amino acid sequence is the hRUP7, an endogenous human orphan  
CC G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned  
CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan  
CC GPCR of the invention, like all GPCRs has seven transmembrane alpha  
CC helices with an extracellular N-terminus and an intracellular C-terminus.  
CC However, no endogenous ligands has yet been identified for the proteins  
CC of the invention. The orphan GPCRs may be used in the identification of  
CC their endogenous ligands, and to screen potential GPCR agonists and  
CC antagonists for use as pharmaceutical agents. The proteins may also be  
CC used in the study of GPCR-mediated signalling cascades, and to elucidate  
CC their precise role in normal and diseased human conditions. Nucleic acid  
CC encoding human orphan GPCRs may be used for tissue localisation  
CC expression analysis to provide information about their function in  
CC healthy and pathological states  
XX  
SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 3; Length 390;  
Best Local Similarity 68.1%; Pred. No. 2.1e-133;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
QY 1 MSESNTGILPPAAQVPLAFILMSSFAFALMVGNAVILAFVVDNLRHRSNYFFNLAI 60  
DB 1 MPDNTNINLSLSTRVTLAFPMSLVAFALMGNALVILAFVVDNLRHRSNYFFNLAI 60  
QY 61 DFLVGLISIPILYIPHLVFNWFGSGICMFWLITDYLCTASVYVNLISYDRYQSVNAV 120  
DB 61 DFFVGVISIPILYIPHTLFEWDFGKEICVFVWLTDTLLCTASVYVNLISYDRYQSVNAV 120  
QY 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMLTASVWNTKDCBPGFVTEWILIT 180  
DB 121 SYRTQHTGVILVIMVAVVILAFVNGPMLTASVWNTKDCBPGFVTEWILIT 178  
QY 181 MLEFLLPVLISVAYFNQIYVSLWKRRALSCPHAGFTTSSASGHLHAGVACTSN 240  
DB 179 SFLEFVPIVLVAFNMNIYVSLWKRRDLSCQHPGLTAVSSNICGHSFGRLSRRSL 238  
QY 241 PGLKESAAHRSSEPRKSSILVSRTHMNSSITAFKVGSPWSESALRQREYAEILRG 300  
DB 239 SASTEVPAFHSERQRRKSSLMFSRTKMNNTIASKMGFSQSDSVALHQREVELLRA 298  
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWFSFNPLY 360  
DB 299 RRLAKSLAILLGFAVCWAPYSLEFIVLSFYSSATGPKSVWYRIAFWLQWFSFNPLY 358  
QY 361 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 391  
DB 359 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 390

RESULT 5  
AAB62445  
ID AAB62445 standard; protein; 390 AA.  
XX  
AC AAB62445;  
XX  
DT 09-JUL-2001 (first entry)  
XX Human GPCR-like polypeptide, PFI-013.  
XX G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;  
KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;  
KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;  
XX signal transduction.  
XX  
OS Homo sapiens.  
XX  
PN EP1096009-A1.

XX 02-MAY-2001.  
XX  
XX 24-OCT-2000; 2000EP-00309364.  
XX  
XX 29-OCT-1999; 99GB-00025641.  
XX 20-APR-2000; 2000GB-00009973.  
XX (PFIZ ) PFIZER LTD.  
XX (PFIZ ) PFIZER INC.  
XX Peter B, O'reilly MA;  
XX WPI; 2001-309854/33.  
XX N-PSDB; AAF83203.  
XX  
XX New G-protein coupled receptor-like polypeptide, polynucleotide for  
PT screening drug candidates for treating diseases associated with signal  
PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.  
XX  
XX Claim 22; Page 44; 66pp; English.

XX This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-  
CC 013, encoded by cDNA of NCIMB 41073. The PFI-013 protein can be expressed  
CC by standard recombinant methodology. Antibodies and modulators of PFI-013  
CC are useful in the manufacture of a medicament for treating allergic  
CC disorder, including extrinsic asthma, immunological disorders, such as  
CC intrinsic asthma, vasculitic granulomatous disease, interstitial and  
CC other pulmonary disease, including chronic obstructive pulmonary disease  
CC (COPD), infectious, inflammatory disease, such as inflammatory bowel  
CC disease and neoplastic and myeloproliferative diseases. They are also  
CC useful for treating obesity, diabetes, metabolic, neurological diseases,  
CC psychotherapeutics, urogenital disease, reproduction and sexual medicine,  
CC inflammation, cancer, tissue repair, dermatology, photoaging, skin  
CC pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases,  
CC allergy and respiratory disease, sensory organ disorders, sleep disorders  
CC and hair loss. The PFI-013 protein and nucleic acid are useful in the  
CC diagnosis and treatment of the above conditions and also for screening  
CC drug candidates for the treatment of diseases associated with signal  
CC transduction. The antibodies are also useful for enrichment of  
CC eosinophils from mammalian, especially human blood and for detecting the  
CC protein in biological samples

SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 4; Length 390;  
Best Local Similarity 68.1%; Pred. No. 2.1e-133;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
QY 1 MSESNTGILPPAAQVPLAFILMSSFAFALMVGNAVILAFVVDNLRHRSNYFFNLAI 60  
DB 1 MPDNTNINLSLSTRVTLAFPMSLVAFALMGNALVILAFVVDNLRHRSNYFFNLAI 60  
QY 61 DFLVGLISIPILYIPHLVFNWFGSGICMFWLITDYLCTASVYVNLISYDRYQSVNAV 120  
DB 61 DFFVGVISIPILYIPHTLFEWDFGKEICVFVWLTDTLLCTASVYVNLISYDRYQSVNAV 120  
QY 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMLTASVWNTKDCBPGFVTEWILIT 180  
DB 121 SYRTQHTGVILVIMVAVVILAFVNGPMLTASVWNTKDCBPGFVTEWILIT 178  
QY 181 MLEFLLPVLISVAYFNQIYVSLWKRRALSCPHAGFTTSSASGHLHAGVACTSN 240  
DB 179 SFLEFVPIVLVAFNMNIYVSLWKRRDLSCQHPGLTAVSSNICGHSFGRLSRRSL 238  
QY 241 PGLKESAAHRSSEPRKSSILVSRTHMNSSITAFKVGSPWSESALRQREYAEILRG 300  
DB 239 SASTEVPAFHSERQRRKSSLMFSRTKMNNTIASKMGFSQSDSVALHQREVELLRA 298  
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWFSFNPLY 360  
DB 299 RRLAKSLAILLGFAVCWAPYSLEFIVLSFYSSATGPKSVWYRIAFWLQWFSFNPLY 358



```
QY 361 PLCHRRFQKAFWKILCVTKWPAISQ-NQSVSS 391
Db 359 PLCHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 6
AAG64477
ID AAG64477 standard; protein; 390 AA.
XX AAG64477;
XX 25-SEP-2001 (first entry)
DT
DE Human G protein-coupled receptor protein BG26.
XX
XX Human; G protein-coupled receptor protein BG26; histamine H3; histamine;
KW altering intracellular cAMP concentration;
KW regulating signal transduction.
XX
XX Homo sapiens.
XX
XX WO200146414-A1.
XX
XX 28-JUN-2001.
XX
XX 20-DEC-2000; 2000WO-JP009038.
XX
XX 20-DEC-1999; 99JP-00361687.
XX
XX (BANY ) BANYU PHARM CO LTD.
XX
XX Itadani H, Nakamura T, Tanaka K, Ohta M;
XX
XX WPI; 2001-441675/47.
XX
XX N-PSDB; AA447911.
XX
XX G protein-coupled receptor protein BG26, with activity of binding to
PT histamine and capable of changing intracellular cAMP concentration in
PT response to its stimulus, applicable as tool in screening ligands or drug
PT candidates.
XX
XX Claim 1; Page 41-44; 50pp; Japanese.
XX
XX The present sequence is that of the human G protein-coupled receptor
CC protein BG26, which shows significant homology with histamine H3, with
CC activity of binding to histamine and capable of changing intracellular
CC cAMP concentration in response to its stimulus. The protein is applicable
CC as a tool in screening ligands or drug candidates for regulating signal
CC transduction from such protein and treating diseases associated with its
CC abnormality
XX
XX Sequence 390 AA;
QY
Query Match 66.9%; Score 1370.5; DB 4; Length 390;
Best Local Similarity 68.1%; Pred. No. 2.1e-133;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
QY 1 MSENSTGLPPAAQVPLAFMSSFAFAIMGVNAVILAFVVDNRHRSNFFFLNLAIS 60
Db 1 MPDTNSTNLSTRVTTLAFMSLVAFALMGNALVILAFVVDNRHRSNFFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHVLENNFNNGSGICMFWLITDYLCTASVYNIIVLISYDRYQSVSNV 120
Db 61 DFFVGVISIPLVPHLTFEWDGKEICVFWLITDYLCTASVYNIIVLISYDRYLSVSNV 120
QY 121 SYRAQHTGMKIVQAVWVILAFVNGPMILASDSWKNSTNTKCEPGFVTEWILITIT 180
Db 121 SYRTQHTGVLKIVTLVAVWVILAFVNGPMILVSESWKDEGS-ECPEPGFSEWILAIT 178
QY 181 MLEFLLPVISVAYENVQIYWSLWKRALSRCPSHAGPSTTSSSAGSHHRAGVACRTSN 240
Db 179 SPLEFVPIVILVAYFNMMIYWSLWKRDLHLSRCQSHPLGTAVSSNICGHSFRGLSSRSL 238
```

```
QY 241 PGLKESAAHSHSRPRKSSILVSLRTHMSSITAFKVGSWFSESAALRQREYAEILRG 300
Db 239 SASTVPASHSRQRKSSLMFSSRTKMNSNTIASKMGFSQSDSVLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSTAFWLQFNFSVNPPLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSPYSATGPKSVWYRIAFWLQFNFSVNPPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPAISQ-NQSVSS 391
Db 359 PLCHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 7
AAB73622
ID AAB73622 standard; protein; 390 AA.
XX AAB73622;
XX
XX 10-AUG-2001 (first entry)
XX
XX Human G protein-coupled receptor AXOR35.
XX
XX AXOR35; human; G protein-coupled receptor; 7TM receptor;
KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;
KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
KW bulimia; osteoporosis; asthma; allergy; urinary retention;
KW acute heart failure; hypotension; hypertension; angina pectoris;
KW myocardial infarction; stroke; ulcer; migraine; vomiting;
KW psychotic disorder; neurological disorder; depression; anxiety; schizophrenia;
KW manic depression; bipolar disorder; dyskinesia; Parkinson's disease;
KW severe mental retardation; Huntington's disease; Gilles de la Tourette's syndrome;
KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
KW macrophage; eosinophil; neutrophil; function modulation;
KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
KW drug screening; signal transduction; transgenic animal; drug discovery.
XX
XX Homo sapiens.
XX
XX WO200133221-A1.
XX
XX 10-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029461.
XX
XX 02-NOV-1999; 99US-00431898.
XX
XX 03-FEB-2000; 2000US-00497790.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Aubart KM, Bergema DJ, Fitzgerald LR, Graybill TL, Li X;
PI Michalovich D, Morrow DM, Zhu Y;
XX
XX WPI; 2001-316464/33.
XX
XX N-PSDB; AA424007.
XX
XX Novel G-protein coupled receptor polypeptide and polynucleotide for
PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological
PT disorders and for identifying modulators useful for treating asthma.
XX
XX Claim 1; Page 50-51; 54pp; English.
XX
XX The invention relates to the human G protein-coupled receptor AXOR35
CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
CC transmembrane domains and is involved in signal transduction. AXOR35 has
CC homology and structural similarity with G protein-coupled receptors such
CC as the human histamine H3 receptor. The invention also relates to
CC expression vectors and host cells comprising AXOR35 DNA, to recombinant
CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins
CC and nucleotides may be used to treat a wide variety of disorders
CC including bacterial, fungal, protozoal and viral infections, particularly
```



CC viral infections, particularly HIV-1 or HIV-2 infections; pain; central  
CC nervous system, neurological and psychotic disorders such as Huntington's  
CC disease, schizophrenia, migraine, depression, anxiety, bipolar disorder,  
CC dementia, Alzheimer's disease, and Parkinson's disease; proliferative  
CC disorders such as cancers, benign prostatic hypertrophy and psoriasis;  
CC metabolic disorders such as diabetes, dyslipidaemia, obesity, and  
CC anorexia; thyroid disorders; cardiovascular diseases such as hypotension,  
CC hypertension, thrombosis, myocardial infarction, cardiomyopathies, and  
CC atherosclerosis; inflammatory conditions; autoimmune disorders (e.g.,  
CC rheumatoid arthritis); hormonal disorders; and renal failure  
XX Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 5; Length 390;  
Best Local Similarity 68.1%; Pred. No. 2.1e-133;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
QY 1 MBSNSTGILPPAAQVPLAFMLSSFAFAMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60  
Db 1 MPDTNSTINLSLSTRVTLAFVSLVAFAMLGNAVLILAFVVDKNLRHRSYFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYVNIIVLSYDRYQSVNAV 120  
Db 61 DFFVGVISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYVNIIVLSYDRYQSVNAV 120  
QY 121 SYRAQHTGIMKIVAOVAVVILAFVNGPMLASDSWKNSTNTKDCPEPGFVTEWYILIT 180  
Db 121 SYRQHTGVILKIVLMAVAVVILAFVNGPMLVSESKDEGS--ECEPGFSEWYILAIT 178  
QY 181 MLEFLLPVISVAYFNVQIYWSLWKRRLSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240  
Db 179 SFLEFVIPVILVAYFNMNIYWSLWKRDLHLSRCQSHPLGTAVSSNICHSFRLSSRRSL 238  
QY 241 PGLKESAAARHSESRRKSSILVSLTHMNSSITAFKVGSMFSESAALRQREYAEILRG 300  
Db 239 SASTVEVPASFHSEQRQRKSSLMFSSRTKMNSTIASKMGFSQSDSVLHQREHVELLRA 298  
QY 301 RKLARSALLLSAFAICWAPYCLFTIVLSTYPTERPKSVYWGYSIAFWLQWNSFVNPLY 360  
Db 299 RRLAKSAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358  
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391  
Db 359 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 390

RESULT 9

ABP98629

ID ABP98629 standard; protein; 390 AA.

XX AC

XX ABP98629;

DT 13-JUN-2003 (first entry)

DE Human histamine receptor SP9144.

XX

XX human; histamine receptor; chromosome 18; anti-inflammatory;

KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;

KW anti-migraine; cardiant; anti-rheumatic; anti-arthritis; antipsoriatic;

KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;

KW myocardial infarction; migraine; chronic obstructive pulmonary disease;

KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;

KW psoriasis; receptor.

XX

OS Homo sapiens.

XX

XX US6204017-B1.

PN 20-MAR-2001.

XX

XX 07-OCT-1999;

XX 99US-00414010.

XX

XX 07-OCT-1999;

XX 99US-00414010.

PR

XX (SCHE ) SCHERING CORP.  
PA Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;  
XX Wang S;  
PI WPI; 2002-442063/47.  
XX N-PSDB; ABZ80663.  
DR  
DR  
XX New nucleic acid encoding antigenic part of human histamine receptor,  
PT useful for preparing antibodies, e.g. for treating-histamine related  
PT disorders.  
XX

Example 1; Col 27-30; 19pp; English.

XX This sequence represents the amino acid sequence of a human histamine  
CC receptor (HR) designated SP9144. The sequence was isolated by searching  
CC databases with the sequence of known G-coupled protein receptor (GPCR).  
CC The gene is used for recombinant production of HR and for preparing  
CC antibodies (Ab). These Ab are used to purify HR by immunoaffinity  
CC chromatography, in immunoassay of histamine receptor, to identify cDNA  
CC clones that express the receptor, as antagonist to block binding of  
CC histamine (for treating any histamine-associated disorder) and to  
CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR  
CC protein can be used in the treatment of e.g. inflammation, asthma,  
CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,  
CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple  
CC sclerosis, inflammatory bowel disease and psoriasis  
XX

Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 5; Length 390;  
Best Local Similarity 68.1%; Pred. No. 2.1e-133;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MBSNSTGILPPAAQVPLAFMLSSFAFAMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60  
Db 1 MPDTNSTINLSLSTRVTLAFVSLVAFAMLGNAVLILAFVVDKNLRHRSYFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYVNIIVLSYDRYQSVNAV 120  
Db 61 DFFVGVISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYVNIIVLSYDRYQSVNAV 120  
QY 121 SYRAQHTGIMKIVAOVAVVILAFVNGPMLASDSWKNSTNTKDCPEPGFVTEWYILIT 180  
Db 121 SYRQHTGVILKIVLMAVAVVILAFVNGPMLVSESKDEGS--ECEPGFSEWYILAIT 178  
QY 181 MLEFLLPVISVAYFNVQIYWSLWKRRLSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240  
Db 179 SFLEFVIPVILVAYFNMNIYWSLWKRDLHLSRCQSHPLGTAVSSNICHSFRLSSRRSL 238  
QY 241 PGLKESAAARHSESRRKSSILVSLTHMNSSITAFKVGSMFSESAALRQREYAEILRG 300  
Db 239 SASTVEVPASFHSEQRQRKSSLMFSSRTKMNSTIASKMGFSQSDSVLHQREHVELLRA 298  
QY 301 RKLARSALLLSAFAICWAPYCLFTIVLSTYPTERPKSVYWGYSIAFWLQWNSFVNPLY 360  
Db 299 RRLAKSAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358  
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391  
Db 359 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 390

RESULT 10

ABB78276

ID ABB78276 standard; protein; 390 AA.

XX AC

XX ABB78276;

XX 05-DEC-2002 (first entry)

XX

XX Amino acid sequence of human histamine receptor.

XX Human; histamine receptor; receptor; inflammation; asthma; allergy;  
 KW atopic dermatitis; stroke; myocardial infection; migraine;  
 KW chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;  
 KW triple sclerosis; inflammatory bowel disease; psoriasis;  
 KW intracellular second messenger pathway; cellular growth rate;  
 KW hormone secretion.

XX Homo sapiens.  
 XX US2002098539-A1.  
 XX 25-JUL-2002.  
 XX 19-MAR-2001; 2001US-00812216.  
 XX 07-OCT-1999; 99US-00414010.  
 XX (BEHA/) BEHAN J X.  
 PA (HEDR/) HEDRICK J A.  
 PA (LAZT/) LAZ T M.  
 PA (MONS/) MONSMA F J.  
 PA (MORS/) MORSE K L.  
 PA (UMLA/) UMLAND S P.  
 PA (WANG/) WANG S.  
 XX Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;  
 PI Wang S;  
 PI Wang S;  
 XX WPI; 2002-673827/72.  
 DR N-PSDB; ABW78739.  
 XX Novel mammalian histamine receptor polypeptide useful for identifying  
 PT agonist or antagonist for treating diseases such as inflammation, asthma,  
 PT stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.  
 XX Claim 2; Page 16-17; 21pp; English.

XX The present sequence represents a histamine receptor. The polypeptide is  
 CC useful for identifying an agonist or antagonist of a mammalian histamine  
 CC receptor. It is useful as an antigen to elicit the production of  
 CC antibodies. The histamine receptor polypeptide and polynucleotide are  
 CC useful in the treatment and management of diseases such as inflammation,  
 CC asthma, allergy, atopic dermatitis, stroke, myocardial infection,  
 CC migraine, chronic obstructive pulmonary disease (COPD), rheumatoid  
 CC arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.  
 CC They are also useful for modulating intracellular second messenger  
 CC pathway activated through histamine receptors (cyclic-AMP, calcium,  
 CC inositol phosphate and mitogen activated protein (MAP) kinase), changes  
 CC in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+  
 CC mobilization, mitogenic effects, etc

XX Sequence 390 AA;  
 SQ

Query Match 66.9%; Score 1370.5; DB 5; Length 390;  
 Best Local Similarity 68.1%; Pred. No. 2.1e-133;  
 Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPIAFIMSSFAFIMVGNVAVIILAFVVDNRLHRSNFFNLAIS 60  
 Db 1 MPDTNSTINLSLSTRVTLFAFFMSLVAFALMLGNALVILAFVVDKRLHRSNFFNLAIS 60  
 QY 61 DFLUGLISIPLYIPIHVLNFWNGSGICMFWLTVDLLCTASVYINVLISYDRYQSVNAV 120  
 Db 61 DFFVGVISIPIYHPTLFEWDFGKEICVFWLTVDLLCTASVYINVLISYDRYQSVNAV 120  
 QY 121 SYRAQHTGIMKTVAQWVAVIILAFVNGPMILASDSWKNSTNTKDCPFGFVTEWILIT 180  
 Db 121 SYRTQHTGVKLVTLMVAVVILAFVNGPMILVSSWKDEGS--SCEPGFFSEWILAIT 178  
 QY 181 MLLEFLLPVISVAYNVQIYWSLWKRRALSRCEPSHAGFTSTSSASGHLHRAQVCRISN 240  
 Db 179 SPLEFVIPVILVAYFMNMIYWSLWKRRDLHSLRCQSHPLGLTAVSSNIGHSFGRLLSRRSL 238

QY 241 PGLKEGAASRHSRPRKSSILVSLRTHMNSSITAFKVSFWRSESAALRQREYAEILLRG 300  
 Db 239 SATEVPASHSERQRKSSLMFSSRTKMSNTIASQWGSFQSDSVALLHQREHVELRA 298  
 QY 301 RKLARSLAILLSAPACWAPYCLFTIVLSTYPTERPKSVYYSIAFWLQWNSFWNPLY 360  
 Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVMYRIAFWLFQWNSFWNPLY 358  
 QY 361 PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS 391  
 Db 359 PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS 390

RESULT 11  
 AAM50564  
 ID AAM50564 standard; protein; 390 AA.  
 XX AC AAM50564;  
 XX 18-MAR-2002 (first entry)  
 XX Human histamine H4 receptor.  
 DE Histamine H4 receptor; human; antiasthmatic; antiallergenic;  
 KW anti-inflammatory; cardiant; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy.  
 XX Homo sapiens.  
 OS WO200192485-A1.  
 PN 06-DEC-2001.  
 PD 22-FEB-2001; 2001WO-US005914.  
 XX 31-MAY-2000; 2000US-0208260P.  
 XX (ORTH ) ORTHO-MCNEIL PHARM INC.  
 PA Lovenberg T, Liu C;  
 PI WPI; 2002-114339/15.  
 DR N-PSDB; AAI70980.  
 XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.

PS Claim 13; Fig 2; 92pp; English.  
 XX The present sequence is that of a human histamine receptor of the H4  
 CC subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA  
 CC library. The invention provides mammalian (human, mouse, rat and guinea  
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the human histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, treating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hypoglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity

XX Sequence 390 AA;  
 SQ

Query Match 66.9%; Score 1370.5; DB 5; Length 390;  
 Best Local Similarity 68.1%; Pred. No. 2.1e-133;  
 Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

```
QY 1 MSEGNTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDNRNLRHRSNYFFLNLAIS 60
Db 1 MPDTNSTINLSLSTRVTLAFMSSLVAFALMGNALVILAFVVDNRNLRHRSNYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLLCTASVYVNIIVLSYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDDYLLCTASVYVNIIVLSYDRYLSVNAV 120
QY 121 SYRAQHTGIMKIVAQVAVILAFVNGPMILASDSWKNSNTKDCBPGFVTEWYILIT 180
Db 121 SYRTQHTGVLKIVTLMAVAVILAFVNGPMLLVSESWKDEGS--ECEPGFSEWYILAIT 178
QY 181 MLEFLLPVISVAYENVQIYWSLWKRRALSRCPHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVPIVILVAYFNNIYWSLWKRDHLSCQSHPGLTAVSSNICGHSFRGLSSRRSL 238
QY 241 PGLKESAAASHSESPPRKSSILYSLRTHMNSSITAFKVGFSWSESAALQREYAEALLRG 300
Db 239 SASTEVPASHSERQRRKSSLMFSSRTKMSNTTASXMGFSQSDSVLHQREHVELLRA 298
QY 301 RKLARSAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFLLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFLLY 358
QY 361 PLCHRRFOKAFWKILCVTKWPALSQ-NQSVSS 391
Db 359 PLCHRRFOKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 12
AAG66023 standard; protein; 390 AA.
AC AAG66023;
XX
XX
DT 27-FEB-2002 (first entry)
XX
DE Human histamine H4 receptor protein.
XX
KW Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;
KW antidiabetic; antiallergic; neuroprotective; antidiabetic; human;
KW cerebroprotective; CAMP modulator; gene therapy.
XX
OS Homo sapiens.
XX
FH Key
FT 12..40
FT Domain
FT /note= "transmembrane domain"
FT 52..69
FT Domain
FT /note= "transmembrane domain"
FT 88..110
FT Domain
FT /note= "transmembrane domain"
FT 130..154
FT Domain
FT /note= "transmembrane domain"
FT 172..196
FT Domain
FT /note= "transmembrane domain"
FT 304..325
FT Domain
FT /note= "transmembrane domain"
FT 342..362
FT Domain
FT /note= "transmembrane domain"
XX
PN WO200185786-A2.
XX
PD 15-NOV-2001.
XX
XX
PF 04-MAY-2001; 2001WO-US014527.
XX
PR 05-MAY-2000; 2000US-0202151P.
PR 23-AUG-2000; 2000US-0227567P.
PR 13-NOV-2000; 2000US-0247855P.
XX
XX
PA (AMHP ) AMERICAN HOME PROD CORP.
XX
```

```
PI Jones PG, Blatcher M, Wu S, Rausch MH;
XX WPI; 2002-049442/06.
DR N-PSDB; AAI67750.
XX
PT New histamine receptor, termed H4 useful for detecting H4 (ant)agonists
PT for treating transplanted organ rejection, asthma, allergy, multiple
PT sclerosis and rheumatoid arthritis.
XX
PS Claim 5; Fig 1; 66pp; English.
XX
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```
CC The invention provides an isolated histamine receptor, H4, which binds
CC ligands comprising imidazole attached to amine by an alkyl chain. The H4
CC receptor can be expressed by standard recombinant methodology. Cells
CC expressing H4 receptor protein at a detectable level can suppress cyclic
CC adenosine monophosphate (cAMP) formation when contacted with the H4
CC receptor agonist. The H4 receptor and antibodies are used for identifying
CC H4 receptor modulators. Modulation of histamine H4 receptors is useful
CC for treating transplanted organ rejection, asthma, allergies and
CC autoimmune pathologies such as multiple sclerosis, type 1 diabetes,
CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor
CC protein and nucleic acids are useful targets to identify drugs that are
CC effective in treating disorders associated with histamine-regulated
CC processes. Identification and isolation of H4 receptor provides for
CC development of screening of molecules that interact with H4 receptors.
CC Genetic variants of H4 can be used to diagnose an H4 associated disease
CC as described above. The H4 receptor polynucleotide is useful to treat or
CC prevent a disorder associated with the function of H4 in peripheral blood
CC leukocytes. The present sequence represents the human histamine H4
CC receptor protein
XX
```

SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 5; Length 390;  
Best Local Similarity 68.1%; Pred. No. 2.1e-133;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

```
QY 1 MSEGNTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDNRNLRHRSNYFFLNLAIS 60
Db 1 MPDTNSTINLSLSTRVTLAFMSSLVAFALMGNALVILAFVVDNRNLRHRSNYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLLCTASVYVNIIVLSYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDDYLLCTASVYVNIIVLSYDRYLSVNAV 120
QY 121 SYRAQHTGIMKIVAQVAVILAFVNGPMILASDSWKNSNTKDCBPGFVTEWYILIT 180
Db 121 SYRTQHTGVLKIVTLMAVAVILAFVNGPMLLVSESWKDEGS--ECEPGFSEWYILAIT 178
QY 181 MLEFLLPVISVAYENVQIYWSLWKRRALSRCPHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVPIVILVAYFNNIYWSLWKRDHLSCQSHPGLTAVSSNICGHSFRGLSSRRSL 238
QY 241 PGLKESAAASHSESPPRKSSILYSLRTHMNSSITAFKVGFSWSESAALQREYAEALLRG 300
Db 239 SASTEVPASHSERQRRKSSLMFSSRTKMSNTTASXMGFSQSDSVLHQREHVELLRA 298
QY 301 RKLARSAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFLLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFLLY 358
QY 361 PLCHRRFOKAFWKILCVTKWPALSQ-NQSVSS 391
Db 359 PLCHRRFOKAFKIFCIKKQPLPSQHSRSVSS 390
```

RESULT 13  
AAU74906  
ID AAU74906 standard; protein; 390 AA.  
XX  
AC AAU74906;  
XX  
DT 09-APR-2002 (first entry)

XX DE Amino acid sequence of human G-protein coupled receptor TGR62 protein.  
XX  
KW Human; G-protein coupled; receptor; GPCR; TGR62; kidney disease;  
KW signal transduction modulator; cerebral cavernous malformation;  
KW hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;  
KW nephritis; hypertension; liver disease; cirrhosis; blood disorder;  
KW spleen-associated disorder; immune disorder.  
XX OS Homo sapiens.  
XX WO200200719-A2.  
XX 03-JAN-2002.  
XX 25-JUN-2001; 2001WO-020363.  
XX 23-JUN-2000; 2000US-0213461P.  
XX (TULA-) TULARIK INC.  
XX Lin DC, Zhao J, Chen J, Cutler G;  
XX N-PSDB; ABK12959.  
XX  
XX New G-protein coupled receptor polypeptides, useful for identifying  
PT modulators of signal transduction for treating kidney disease,  
PT hyperlipidemia, obesity, dyslexia and cardiac myxoma.  
XX  
XX Claim 26; Page 61; 78pp; English.  
XX  
XX The present invention relates to a new G-protein coupled receptor (GPCR)  
CC polypeptide comprising greater than 70% amino acid sequence identity to  
CC the amino acid sequence of human GPCRs TGR62, TGR130.1, TGR130.2,  
CC human TGR123 or TGR92, 80% amino acid sequence identity to mouse TGR18 or  
CC 90% amino acid sequence identity to human novel edg receptor protein, as  
CC defined in the specification. The GPCR covalently linked to a solid phase  
CC is useful for identifying a compound that modulates signal transduction.  
CC The identified compounds are useful for treating kidney disease, cerebral  
CC cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac  
CC myxoma. The molecules of the invention are useful for diagnosing  
CC disorders or conditions such as kidney-related conditions or diseases  
CC such as renal failure, nephritis, nephrotic syndrome, asymptomatic  
CC urinary abnormalities, renal tubule defects, hypertension and  
CC nephrolithiasis, liver-related disease or condition e.g. cirrhosis,  
CC infiltrations, lesions, functional disorders and jaundice and spleen-  
CC associated disorders or conditions e.g. splenic enlargement, immune  
CC disorders, blood disorders and others. Modulation of the polypeptide of  
CC the invention is useful to treat or prevent any of the above conditions  
CC or diseases. The present amino acid sequence represents the human GPCR  
CC TGR62 protein of the invention. This sequence is one of seven novel G  
CC protein coupled receptors of the invention (AAU74904- AAU74911)  
XX Sequence 390 AA;  
SQ  
Query Match 66.9%; Score 1370.5; DB 5; Length 390;  
Best Local Similarity 68.1%; Pred. No. 2.1e-133;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
QY 1 MSENSTGLIPPAQVPLAFMLSSPAFALMGVNAVILAFVVDRLHRHSNYFFLNLAIS 60  
Db 1 MPDTNSTINLSLSTRVTLFAFFMSLVAFALMLGNALVILAFVVDKRLHRSSYFFLNLAIS 60  
QY 61 DFLVGLISLPIPHVFNWNGSGICMPWLITDYLCTASVYNIIVLISYDRYSVNAV 120  
Db 61 DFFVGVISLPIPHVFNWNGSGICMPWLITDYLCTASVYNIIVLISYDRYSVNAV 120  
QY 121 SYRAOHTGIMKVAQWVAVILAFVNGPMILASDSWKNSTNTKDCPGFVTEWYLTIT 180  
Db 121 SYRTQHTGIMKIVLAVVAVILAFVNGPMILVSVESWKEGS--EECPGFSEWYLTIT 178  
QY 181 MLLEFLPLVISVAYFNQVYVQVLSLWKRRALSRCPFHAGFTTSSASGHLHRAVACRTSN 240

Db 179 SFLEFVIPVILVAYFNWNIYSLWKRDHLSCOSHPGLTAVSSNICHSFGRUSRRSL 238  
QY 241 PGLKESASRHSRSPREKSSILVLRTHMNSSITAFKVGSRFMRSESAALRQREYAEILRG 300  
Db 239 SASTEPASPHSERQRKSSLMFSSRTYKMSNTTASKMGFSQSDSVALLHQREHVELLRA 298  
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTEREKSVMYSIAFWLQWNSFVNPLY 360  
Db 299 RRLAKSLAILLGFAVCWAPYSLFTIVLSFYSSATGPKSVMYRIAFWLNFSFVNPLY 358  
QY 361 PLCHRRFQKAPFKILCVTKWPAISO-NQSVSS 391  
Db 359 PLCHRRFQKAPFKILCVTKWPAISO-NQSVSS 390  
RESULT 14  
ABG71960 standard; protein; 390 AA.  
XX ID ABG71960;  
XX AC ABG71960;  
XX DT 28-JAN-2003 (first entry)  
XX DE Human G-protein coupled receptor AXOR35.  
XX KW Human; receptor; G-protein coupled receptor; AXOR35; lymphocyte;  
KW macrophage; eosinophil; neutrophil; infection; transplant rejection;  
KW gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;  
KW Crohn's disease; irritable bowel syndrome; vomiting; inflammation;  
KW atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;  
KW psoriasis; urological disease; urinary retention; cardiovascular disease;  
KW myocardial infarction; hypotension; hypertension; pulmonary disorder;  
KW renal ischaemia; arteriosclerosis; atherosclerosis; psychosia;  
KW chronic obstructive pulmonary disease; cough; renal disease;  
KW neurological disorder; migraine; anorexia; anxiety; schizophrenia;  
KW dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;  
KW graft versus host disease; osteoporosis.  
XX OS Homo sapiens.  
XX US2002137054-A1.  
XX 26-SEP-2002.  
XX 20-JUL-2001; 2001US-00910411.  
XX 02-NOV-1999; 99US-00431898.  
XX 03-FEB-2000; 2000US-00497790.  
XX 20-OCT-2000; 2000US-00693761.  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX Aubart KM, Bergema DJ, Fitzgerald L, Graybill TL, Li X;  
PI Michalovich D, Morrow DM, Zhu Y;  
DR WPI: 2003-074982/07.  
DR N-PSDB; ABS57063.  
XX Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for  
PT treating infections, gastrointestinal disorders, autoimmune disorders,  
PT urological diseases, cardiovascular diseases and cancer.  
XX Claim 1; Page 22; 24pp; English.  
XX The invention relates to an isolated G-protein coupled receptor  
CC polypeptide, AXOR35, (and its homologues and variants) and its encoding  
CC polynucleotide (and its homologues, variants, complements and RNA  
CC equivalents). Also included are an anti-AXOR35 antibody, an AXOR35  
CC expression vector, producing a recombinant host cell by introducing the  
CC vector into a cell, such that the host cell produces AXOR35, a membrane of  
CC the host cell expressing AXOR35, identifying/screening for agonists or

CC antagonists of AXOR35 and inhibiting or promoting the function of  
 CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,  
 CC by administering to the patient AXOR35 agonists or antagonists. The  
 CC agonist or antagonist identified is useful for treating a disease such as  
 CC asthma, or for inhibiting or promoting the function of lymphocytes,  
 CC macrophages, eosinophils, or neutrophils in diseased tissue such as an  
 CC asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays,  
 CC for identifying compounds that are agonists or antagonists of AXOR35, as  
 CC vaccines, or for treating infections (bacterial, fungal, protozoan or  
 CC viral infections), transplant rejection, gastrointestinal disorders (such  
 CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),  
 CC irritable bowel syndrome, vomiting, inflammation (such as atopic  
 CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,  
 CC psoriasis), neurological diseases (such as urinary retention), hypotension,  
 CC cardiovascular diseases (such as myocardial infarction), hypertension,  
 CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary  
 CC disease), cough, renal diseases (such as renal ischaemia),  
 CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders  
 CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such  
 CC as Parkinson's disease), cancer, obesity, stroke, septic shock, graft  
 CC versus host disease and osteoporosis. The present sequence represents  
 CC human AXOR35  
 XX  
 SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 6; Length 390;  
 Best Local Similarity 68.1%; Pred. No. 2.1e-133;  
 Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVDRNLHRNSYFFLNLAIS 60  
 Db 1 MPTDNTINLSLSTRVTLAFMSSVLAFAIMLGNALVILAFVDRNLHRNSYFFLNLAIS 60  
 QY 61 DFLVGLISIPLYIPIHVLFWNNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVNAV 120  
 Db 61 DFFVGVISIPLYIPIHVLFWNDPKEICVFWLITDYLLCTASVYNIVLISYDRYLSVNAV 120  
 QY 121 SYRAQHTGIMKIVAQMVAVVILAFVNGPMLASDSWKNSINTKDCPPGVTEWYILIT 180  
 Db 121 SYRTQHTGVILKIVLMVAVVILAFVNGPMLVSESKWDEGS--ECEPGFFSEWYILAIT 178  
 QY 181 MLLEFLLPVISVAVNVQIVWSIKRALSRCPSHAGFTSTSSASGHLHRAGVARTSN 240  
 Db 179 SLEFVIVPILVAYFNNIYWSLWKRDHLSRCQSHPLGTAVSSNICCHSPRGRLSRRSL 238  
 QY 241 PGLKESAAHRHSDSPRRKSSILVSLTHMNSSITAFKGVSWFSESAALRQREYAILRG 300  
 Db 239 SASTVPASFHSEQRQRKSLMFSSTKNSNTIASKMGFSOSDSVALHQREHVELLRA 298  
 QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360  
 Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLOWNSFVNPFY 358  
 QY 361 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 391  
 Db 359 PLCHRRFQKAFILKIFCIKQPLFSQHSRVS 390

RESULT 15

ID ABU92265

XX ABU92265 standard; protein; 390 AA.

AC ABU92265;

XX

DT 16-JUL-2003 (first entry)

XX

DE Human G protein-coupled receptor hRUP7.

XX

KW Human; receptor; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;  
 KW hARE-5; hRUP3; hRUP5; hRUP6; hRUP7; hGPCR27; hARE-1; hARE-2; hRUP1; hG2A;  
 KW hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hRUP4; signalling cascade.

OS Homo sapiens.

XX  
 EN US2003017528-A1.  
 XX  
 PD 23-JAN-2003.  
 XX  
 PF 06-JUN-2001; 2001US-00875076.  
 XX  
 PF 20-NOV-1998; 98US-0109213P.  
 XX 16-FEB-1999; 99US-020416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123949P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.  
 PR 28-MAY-1999; 99US-0136567P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 29-JUN-1999; 99US-0141448P.  
 PR 28-SEP-1999; 99US-0156333P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 12-OCT-1999; 99US-00417044.  
 XX  
 PA (CHEN/) CHEN R.  
 PA (DANG/) DANG H T.  
 PA (LIAN/) LIAN C W.  
 PA (LINI/) LIN I.  
 XX  
 PI Chen R, Dang HT, Liaw CW, Lin I;  
 XX  
 XX WPI: 2003-428952/40.  
 DR N-PSDB; ACA93262.  
 DR  
 XX Novel endogenous, orphan, human G protein-coupled receptors useful for  
 PT identification of modulators of the receptor and as research tools for  
 PT understanding the role of the receptor in human body.  
 PT  
 PS Claim 26; Page 23; 54pp; English.  
 XX  
 CC The invention relates to a human G protein-coupled receptor (GPCR)  
 CC appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named  
 CC hARE-3, hARE-4, hARE-5, hRUP3, hRUP5, hRUP6, hRUP7, hGPCR27, hARE-1, hARE  
 CC -2, hRUP1, hG2A, hCHN3, hCHN4, hCHN6, hCHN8, hCHN9, hCHN10 and hRUP4.  
 CC Also included are a plasmid comprising a vector and one of the cDNAs  
 CC above and a host cell comprising the plasmid. The GPCRs are useful for  
 CC the direct identification of candidate compounds as inverse agonists,  
 CC agonists or partial agonists. In vitro and in vivo systems incorporating  
 CC GPCRs is useful for elucidating and understanding the roles these  
 CC receptors play in the human condition, both normal and diseased, as well  
 CC as understanding the role of constitutive activation as it applies to  
 CC understanding the signalling cascade. The cDNAs are useful for making a  
 CC probe for dot-blot analysis against tissue mRNA and/or RT-PCR  
 CC identification of the expression of the receptor in tissue samples. The  
 CC present sequence represents a GPCR of the invention  
 XX  
 SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 6; Length 390;  
 Best Local Similarity 68.1%; Pred. No. 2.1e-133;  
 Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVDRNLHRNSYFFLNLAIS 60  
 Db 1 MPTDNTINLSLSTRVTLAFMSSVLAFAIMLGNALVILAFVDRNLHRNSYFFLNLAIS 60  
 QY 61 DFLVGLISIPLYIPIHVLFWNNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVNAV 120  
 Db 61 DFFVGVISIPLYIPIHVLFWNDPKEICVFWLITDYLLCTASVYNIVLISYDRYLSVNAV 120  
 QY 121 SYRAQHTGIMKIVAQMVAVVILAFVNGPMLASDSWKNSINTKDCPPGVTEWYILIT 180  
 Db 121 SYRTQHTGVILKIVLMVAVVILAFVNGPMLVSESKWDEGS--ECEPGFFSEWYILAIT 178

Mon Oct 4 10:27:27 2004

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Db	239	SASTEVPASPHSERQRRKSSIMFSSRTKMNSNTIASKMGFSQSDSVLHQREHVELLA	298
QY	301	RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPLY	360
Db	299	RRLAKSLAILLGVEAVCWAPYSLFTIVLSFYSSATGPKSVWYRTAFWLQWFNSFVNPLY	358
QY	361	PLCHRRRQKAFWKILCVTKWPAISO-NOSVSS	391
Db	359	PLCHRRRQKAFWKILCVTKWPAISO-NOSVSS	390

Search completed: October 1, 2004, 10:11:32  
Job time : 64 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 1, 2004, 10:10:33 ; Search time 18 Seconds  
(without alignments)  
1121.431 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPALESQNSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/prodata/2/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/prodata/2/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/prodata/2/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/prodata/2/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/prodata/2/iaa/PCUS COMB.pep.\*
- 6: /cgn2\_6/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1370.5	66.9	390	3	US-09-414-010-2
2	1370.5	66.9	390	4	US-09-812-216-2
3	722.5	35.3	445	2	US-08-985-090-2
4	722.5	35.3	445	3	US-09-165-543-2
5	722.5	35.3	445	3	US-09-167-354-7
6	722.5	35.3	445	4	US-09-642-855-7
7	722.5	35.3	445	4	US-09-642-514-7
8	716.5	35.0	445	3	US-09-165-543-5
9	621.5	30.3	351	4	US-09-524-162-2
10	582.5	28.4	362	2	US-08-985-090-5
11	582.5	28.4	362	3	US-09-165-543-32
12	427	20.8	348	1	US-08-118-270-13
13	427	20.8	348	5	PCUS-093-08528-13
14	427	20.8	355	1	US-08-118-270-11
15	427	20.8	355	5	PCUS-093-08528-11
16	415.5	20.3	479	1	US-08-313-553-7
17	415.5	20.3	479	3	US-08-767-993-7
18	393	19.2	354	1	US-08-313-553-9
19	393	19.2	354	3	US-08-767-993-9
20	390.5	19.1	501	1	US-08-722-001-14
21	390.5	19.1	501	2	US-08-467-568-9
22	390.5	19.1	501	2	US-09-030-582-9
23	389.5	19.0	513	3	US-08-406-855A-21
24	389.5	19.0	513	3	US-09-206-899-21
25	389.5	19.0	515	1	US-08-444-734A-7
26	389.5	19.0	515	2	US-08-406-855A-22
27	389.5	19.0	515	3	US-09-206-899-22

28	388.5	19.0	572	1	US-08-334-698-2	Sequence 2, Appli
29	388.5	19.0	572	1	US-08-328-932-2	Sequence 2, Appli
30	388.5	19.0	572	1	US-08-468-939-2	Sequence 2, Appli
31	388.5	19.0	572	1	US-08-722-001-30	Sequence 30, Appli
32	388.5	19.0	572	2	US-08-406-855A-2	Sequence 2, Appli
33	388.5	19.0	572	2	US-08-722-190-2	Sequence 2, Appli
34	388.5	19.0	572	3	US-08-244-354-2	Sequence 2, Appli
35	388.5	19.0	572	3	US-09-206-899-2	Sequence 2, Appli
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37	388.5	19.0	572	4	US-09-688-415-2	Sequence 2, Appli
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39	388.5	19.0	572	5	PCT-US95-04203-2	Sequence 2, Appli
40	387.5	18.9	515	4	US-09-688-415-9	Sequence 9, Appli
41	386.5	18.9	515	1	US-08-722-001-25	Sequence 5, Appli
42	385.5	18.8	515	3	US-09-032-742-5	Sequence 10, Appli
43	385.5	18.8	559	2	US-08-406-855A-20	Sequence 20, Appli
44	385	18.8	559	3	US-09-206-899-20	Sequence 20, Appli
45	385	18.8	559	3	US-09-206-899-20	Sequence 20, Appli

ALIGNMENTS

RESULT 1  
US-09-414-010-2  
; Sequence 2, Application US/09414010  
; Patent No. 6204017  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monsma, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414,010  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-414-010-2

Query Match	66.9%	Score	1370.5	DB	3	Length	390
Best Local Similarity	68.1%	Pred. No.	7.2e-106				
Matches	267	Conservative	40	Mismatches	82	Indels	3
Gaps	2						
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Db	1	MDPTNTINLSLSTRVTTLAFMSLVAFALMGLNALVILAFVVDKRLHRSSYFFLNLAIS	60				
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QY	181	MLLEFLLPVIIVAVFNQIYWSLMKRRALRCPHAGFTSSSSAGSHLHAGVACRTSN	240				
Db	179	SFLEFVIVILVAVFNQIYWSLMKRRALRCPHAGFTSSSSAGSHLHAGVACRTSN	238				
QY	241	PGLKESARSHSEPRKXSSILVSLRTHMSSITAFKVGSWRSEAAALROREVAELRG	300				
Db	239	SASTVEPASFHSEQRKXSSLMFSRTTMMNSNTIASKMGFSQSDSVLHOREHVELRA	298				
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Db	301	RKLARSIALLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFWNPFLY	360				

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QY 361 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 391  
Db 359 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 390  
RESULT 2  
US-09-812-216-2  
; Sequence 2, Application US/09812216  
; Patent No. 6613533  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monima, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/812.216  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 09/414,010  
; PRIOR FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-812-216-2

Query Match 66.9%; Score 1370.5; DB 4; Length 390;  
Best Local Similarity 68.1%; Pred. No. 7.2e-106;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
QY 1 MSENSTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNLRHRSYFFFLNLAIS 60  
Db 1 MPDNTNINLSLSTRTVLAFFMSLVAFAMIGNALVILAFVVDNLRHRSYFFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYNIIVLSYDRYOSVNAV 120  
Db 61 DFFVGVSIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYNIIVLSYDRYOSVNAV 120  
QY 121 SYRAQHTGIMKIVAQWAVILAFVNGPMILASDSWKNSTNTKDCPCGFVTEWILIT 180  
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QY 181 MLLEFLPLVIVAVENVOIYVSLMKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240  
Db 179 SFLEFVPIVILVAVENVOIYVSLMKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 238  
QY 241 PGLKESAAHSESPRRKSSILVLSRTHMNSSITAFKVGSEFWRSESAALQREYAEALRG 300  
Db 239 SASTEVPAFSEHQRKSSLMFSRSTKNSNTIAKMGFSQSDSVALHQREHVELLRA 298  
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Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNQSVNPLLY 358  
QY 361 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 391  
Db 359 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 390

RESULT 3  
US-08-985-090-2  
; Sequence 2, Application US/08985090  
; Patent No. 5885893  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl  
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR

; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,090  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jean M. Silveri  
; REGISTRATION NUMBER: 39,030  
; REFERENCE/DOCKET NUMBER: MNI-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-985-090-2

Query Match 35.3%; Score 722.5; DB 2; Length 445;  
Best Local Similarity 38.8%; Pred. No. 4e-52;  
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;  
QY 18 LAFUMSSGFAFAMVGNVILAFVVDNLRHRSYFFFLNLAISDFLVGLISIPLYIPHLV 77  
Db 37 LAALMALLIVATVIGNALVILAFVADSLRTQNNFFLLNLAISDFLVGAFCLPLVVPYL 96  
QY 78 F-NNPFGSGICMFWLITDYLCTASVYNIIVLSYDRYOSVNAVSYRAQHTGIMKIVAO 136  
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLSYDRFLSVTRAVSYRAQQGDTTRAVRKM 156  
QY 137 VAVMILAFVNGPMILASDSWK-----NSTNTKDCPCGFVTEWILITITLLEFLPLVIS 191  
Db 157 LLVWVLAFLLYGPAIL-----SWEYLSGGSSIPEGHCYAEFFYNWIFLITASTLEFPTFELS 213  
QY 192 VAVENVOIY-----WSLWKRRLSRCPSH 215  
Db 214 VTFNLSIYLIQRIQLDGLAREAGPEPPPAQSPPPPPGCGWQCGHGEAMPLH 273  
QY 216 -----AGFTSTSSASGHLHRAGVACRTSNPGLKESAAHSESPRRKSSILV 263  
Db 274 RYGVGEAAVGAEGEATLGGGGG-----GSVASPTSSSG-----SSRGTETPR----- 318  
QY 264 SLRTHMNSSITAFKVGSEFWRSESAALROR-----EYAEFLRGRKLARSAILLSAF 314  
Db 319 -----SLKRGSKPSASSASLEKRMKMSQSFQRFSLDRDKVAKSLAVIVSIF 367  
QY 315 AICWAPYCLFTIVLSTPRTERPKSVVYISIAFWLQWFNQSVNPLLYIPCHRRFQKAFWKI 374  
Db 368 GLCWAPYTLMLIRAAACHGCV-P-DYWYETSFLLWANSVAVNPVLYPLCHHSFRFAFTKL 426  
QY 375 LCVTK 379  
Db 427 LCPQK 431  
RESULT 4  
US-09-165-543-2

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Db          427 LCPQK 431  
|| |  
  
RESULT 5  
US-09-167-354-7  
; Sequence 7, Application US/09167354A  
; Patent No. 6136559  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: SUBTYPE  
; CURRENT APPLICATION NUMBER: US/09/167,354A  
; CURRENT FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE  
US-09-167-354-7  
  
Query Match      35.3%; Score 722.5; DB 3; Length 445;  
Best local Similarity 38.8%; Pred.No. 4e-52;  
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;  
  
QY   18 LAFLMSFAFAlMGNAVVILAFVDENLRHSNYFFNLNLAISDFLVGLISIPLYIPIHVL 77  
    ||| : :::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||  
DB   37 LAALMALLIVATVIGNALVMIAFVAOSSLTQNFFLLNLAISDFLVGFACIPLYVPYL 96  
    ||| : :::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||  
  
QY   78 F-NWFGSGICMEWLITDYLLCTASVYNVILI SYDRYSVSNAVSYRAOHTGIMKI VAO 136  
    ||| : :::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||  
DB   97 TGRWTFRGLCKLWVDDYLLCTSSAFNVILISYDRLSVTRAVSYPAAQQGDTRAVRKM 156  
    ||| : :::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||  
  
QY   137 VA WII AFLVNGPM I LASDWK-----NSNTNKDCBPGFVTWEWILTMLLEFLLPVIS 191  
    ||| : :::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||  
DB   157 LLVNWILAFLYLGAIL---SWEYLSGGSSIPEGHCYAFFFFNNVFYTASTLEFFTFFLS 213  
    ||| : :::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||  
  
QY   192 VAYFNVOIQ-----WSLKWRALSRCPSH 215  
    ||| : :::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||  
DB   214 VI FFNLSI YINIRTLRD LGAREAGP PPPPAQPSPPPPCGWCGWKGHGEAMPLH 273  
    ||| : :::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||  
  
QY   216 -----AGFTTSSASH LR AGVACTRNPL KESAARSHSES PRKGSI LV 263  
    ||| : :::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||  
DB   274 RYGVGEA AVGA E ATLOGGGG----GSVASPTS SG-----SSRGTERPR----- 318  
    ||| : :::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||  
  
QY   264 SLRTHNMSSIT AFKVCSFWRS S ALQR-----EYAEILLRK GKARSIALILLSAF 314  
    ||| : :::||:::||:::||:::||:::||:::||:::||:::||~::~||:::||:::||  
DB   319 -----SLKRGSKFSA SAS LEKRMKWVS QSF TOR FL SRDKVKAKSLAVIVSIF 367  
    ||| : :::||:::||:::||:::||:::||:::||~::~||:::||:::||:::||  
  
QY   315 ALCWAPYC LTFTVLSTPYRTEPKSVWYSIA FWLNFSVNPF LP LCHRRFKQA FWKI 374  
    ||| : :::||:::||:::||:::||:::||:::||~::~||:::||:::||:::||  
DB   368 GLCWAPY TLMI IRACHGC VP-DIWYET SF WL LMANS AVNP VL PL CHHS FRRAFTKL 426  
    ||| : :::||:::||:::||:::||:::||:::||~::~||:::||:::||:::||  
  
QY   375 LC VKT 379  
    ||| : :::||:::||:::||:::||:::||:::||~::~||:::||:::||:::||  
DB   427 LCPQK 431
```

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; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-642-855-7

Query Match      35.3%; Score 722.5; DB 4; Length 445;
Best Local Similarity 38.8%; Pred. No. 4e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFLMSFAPAIMVGNNAVILAFVVDRLNRHRSNYFFLNLAISDFLVGLSIPYIPHYVL 77
DB 37 LAALMALLIVATVIGNALVMAFAVDSSLRQTQNNFFLNLAISDFLVGAFCIPLYVPEYL 96
QY 78 F-NWNFGSGICMFWLITDYLLCTASVYNIIVLISVDYQSVSNVSVYRAQHTGIMKIVAOM 136
DB 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIIVLISYDRFLSVTRAVSYRAQOQDTRAVRKM 156
QY 137 VAVMILAFVNGPMILASDSWK-----NSTNTKDCPEGFVTEWYILITMLLEFLLEVIS 191
DB 157 LLVWVLAFLYGPAIL---SWEYLSGSSSIPEGHCYAEFFNWFYLLITASTLEFFTFPLS 213
QY 192 VAYFNVOIY-----WSLWKRRLSRCPSH 215
DB 214 VTFFNLSTIYLNIOQRTRLRDLGAREAGPEPPPEAQPSPPPPCGWCQKQGHGEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESASRHSSESPPRKSILV 263
DB 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG-----SSSRGTERPR 318
QY 264 SLRTHMNSSITAPKVGFWSESAALRQ-----EYAEELRGRKLARSAILLSAF 314
DB 319 -----SLKRGKPSASSASLEKRMKWSQSFTQRFRLSRDRKVAKSIAVVISIF 367
QY 315 AICWAPYCLFTIVLSTYPTERTPKSVWYSIAFWLQWNSFNPNPLYLCHRRFOKAFWKI 374
DB 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLYPLCHHSFRRFPTKL 426
QY 375 LCVTK 379
DB 427 LCPQK 431

RESULT 7
US-09-642-514-7
; Sequence 7, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-642-514-7

Query Match      35.3%; Score 722.5; DB 4; Length 445;
Best Local Similarity 38.8%; Pred. No. 4e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFLMSFAPAIMVGNNAVILAFVVDRLNRHRSNYFFLNLAISDFLVGLSIPYIPHYVL 77
DB 37 LAALMALLIVATVIGNALVMAFAVDSSLRQTQNNFFLNLAISDFLVGAFCIPLYVPEYL 96
QY 78 F-NWNFGSGICMFWLITDYLLCTASVYNIIVLISVDYQSVSNVSVYRAQHTGIMKIVAOM 136
DB 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIIVLISYDRFLSVTRAVSYRAQOQDTRAVRKM 156
QY 137 VAVMILAFVNGPMILASDSWK-----NSTNTKDCPEGFVTEWYILITMLLEFLLEVIS 191
DB 157 LLVWVLAFLYGPAIL---SWEYLSGSSSIPEGHCYAEFFNWFYLLITASTLEFFTFPLS 213
QY 192 VAYFNVOIY-----WSLWKRRLSRCPSH 215
DB 214 VTFFNLSTIYLNIOQRTRLRDLGAREAGPEPPPEAQPSPPPPCGWCQKQGHGEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESASRHSSESPPRKSILV 263
DB 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG-----SSSRGTERPR 318
QY 264 SLRTHMNSSITAPKVGFWSESAALRQ-----EYAEELRGRKLARSAILLSAF 314
DB 319 -----SLKRGKPSASSASLEKRMKWSQSFTQRFRLSRDRKVAKSIAVVISIF 367
QY 315 AICWAPYCLFTIVLSTYPTERTPKSVWYSIAFWLQWNSFNPNPLYLCHRRFOKAFWKI 374
DB 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLYPLCHHSFRRFPTKL 426
QY 375 LCVTK 379
DB 427 LCPQK 431

RESULT 8
US-09-165-543-5
; Sequence 5, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-165-543-5

Query Match      35.0%; Score 716.5; DB 3; Length 445;
Best Local Similarity 40.2%; Pred. No. 1.3e-51;
Matches 165; Conservative 54; Mismatches 128; Indels 63; Gaps 10;

QY 18 LAFLMSSFAFALMGNVAVILAFVVDNRNLHRSNYFFLNLAISDFLVGLISIPLYIPHL 77
Db 37 LAALMALLIVATVLGNALVLMFAFVADSSLRTONFFLNLAISDFLVGAFICPLYPVPL 96

QY 78 F-NWNFGSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVNNAVSYRAOHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLMLVVDYLLCASSVFNIVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156

QY 137 VAVWILAFVNGPMLASDSWK-----NSTNTKDCPEGFVTEWYILITITMLLEFLPLVIS 191
Db 157 ALVWILAFVLYGPAIL---SWEYLSGSGSIPEGHCVAFYFNWYFLITASTLEFFTPFLS 213

QY 192 VAVFNQIYWSLWKRAL-----SRCPSHAGFTSTSSASGH-----LH 230
Db 214 VTFNLSIVLNIOQRTLRLLDGGREGAPPPPPAPPPSCWCKGHEAMPLH 273

QY 231 RAGVACRTNPNGLK-----ESAASRHSERPRKSSILVSLRTHM 269
Db 274 RYGVG--EAGPGVEAGEALGGSGGGAASPTSSGSSSRGTERPR-----SLKRG 324

QY 270 NSGITAFKVGSWFWSAALRQREYAEALLRGRKLARSALILSAFAICWAPYCLFTIVLS 329
Db 325 KPSASASLEKMKMYSQISQITQ--FRLSDDKKVAKSLAIVSIFGLCWAPYTLMLIIRA 382

QY 330 TYPRTERPKSVWYSIAFWLQWNSFNPNFLYPLCHRRFQKAFWKILCVTK 379
Db 383 ACHGRICP-DYWYETSFLLWANSVAVNPVLYPLCHYSFRRAFTKLLCPQK 431

RESULT 9
US-09-524-162-2
; Sequence 2, Application US/09524162
; Patent No. 6355452
; GENERAL INFORMATION:
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: HUMAN HISTAMINE H3 GENE VARIANT-2
; CURRENT APPLICATION NUMBER: US/09/524,162
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-524-162-2

Query Match      30.3%; Score 621.5; DB 4; Length 351;
Best Local Similarity 38.3%; Pred. No. 7.1e-44;
Matches 141; Conservative 44; Mismatches 110; Indels 73; Gaps 8;

QY 18 LAFLMSSFAFALMGNVAVILAFVVDNRNLHRSNYFFLNLAISDFLVGLISIPLYIPHL 77
Db 37 LAALMALLIVATVLGNALVLMFAFVADSSLRTONFFLNLAISDFLVG----- 84

; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-165-543-5

Query Match      28.4%; Score 582.5; DB 2; Length 362;
Best Local Similarity 37.7%; Pred. No. 1.3e-40;
Matches 137; Conservative 45; Mismatches 118; Indels 63; Gaps 10;

QY 65 GLISIPLYIPHLVLF-NWNFGSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVNNAVSYR 123
Db 1 GAFICPLYPVPLVGRWTFGRGLCKLMLVVDYLLCASSVFNIVLISYDRFLSVTRAVSYR 60

; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-985-090-5

Query Match      28.4%; Score 582.5; DB 2; Length 362;
Best Local Similarity 37.7%; Pred. No. 1.3e-40;
Matches 137; Conservative 45; Mismatches 118; Indels 63; Gaps 10;

QY 65 GLISIPLYIPHLVLF-NWNFGSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVNNAVSYR 123
Db 1 GAFICPLYPVPLVGRWTFGRGLCKLMLVVDYLLCASSVFNIVLISYDRFLSVTRAVSYR 60
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1 GAPCIPLVYVYLTGRWTFGRGLCKLWVVDYLLCASSVFNVLISYDRFLSVTRAVSYR 60  
124 AQTGIMKIVAQWAVWILAFVNGPMILASDWK-----NSTNTKDCBPGFVTEWYILT 178  
61 AQOQDTRRAVRKMAVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCHYAEFFYNWYFLI 117  
179 ITMLBFLPLVIVAVFNVQIYWSLWKRRAL-----SRCPSHAGFSTTS 222  
118 SASTLEFFTFPLSVTFNLSIYLNIOQRTRLRLDGGREGAPPPDDAQPPPPAPPSCWG 177  
223 SSASGH-----LHRAGVACRTSNPGLK-----ESAASHSESPR 256  
178 CWPKGHEAMPLHRYGVG--EAGPGVEAGEAALGGGGGGAASPTSSSGSSRGTERPR 235  
257 RKSILVSLRTHMNSSITAFKVGFSWSESAALRQREYAEILLRGRKLARSILAILLSAPAI 316  
236 -----SLKRGKSPSASSASLEKRMKWVSQISQIR--FRLSRDKKVAKSLAIVSIFGL 286  
317 CWAPYCLFTIVLSTYPTERPKSVWYSIAFWLWNSFVNPFLYPLCHRRFQKAFWKILC 376  
287 CWAPYTLMLTIRAACHGRCIP-DYWYETSFLLWANSVAVNPVLYPLCHYSFRRAFTKLLC 345  
377 VTK 379  
346 PQK 348

RESULT 12  
US-08-118-270-13  
; Sequence 13, Application US/08118270  
; Patent No. 5508384  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Randall B.  
; APPLICANT: Schuster, David I.  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/118,270  
; FILING DATE: 09-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY-2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 348 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-118-270-13

124 AQTGIMKIVAQWAVWILAFVNGPMILASDWK-----NSTNTKDCBPGFVTEWYILT 178  
61 AQOQDTRRAVRKMAVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCHYAEFFYNWYFLI 117  
179 ITMLBFLPLVIVAVFNVQIYWSLWKRRAL-----SRCPSHAGFSTTS 222  
118 SASTLEFFTFPLSVTFNLSIYLNIOQRTRLRLDGGREGAPPPDDAQPPPPAPPSCWG 177  
223 SSASGH-----LHRAGVACRTSNPGLK-----ESAASHSESPR 256  
178 CWPKGHEAMPLHRYGVG--EAGPGVEAGEAALGGGGGGAASPTSSSGSSRGTERPR 235  
257 RKSILVSLRTHMNSSITAFKVGFSWSESAALRQREYAEILLRGRKLARSILAILLSAPAI 316  
236 -----SLKRGKSPSASSASLEKRMKWVSQISQIR--FRLSRDKKVAKSLAIVSIFGL 286  
317 CWAPYCLFTIVLSTYPTERPKSVWYSIAFWLWNSFVNPFLYPLCHRRFQKAFWKILC 376  
287 CWAPYTLMLTIRAACHGRCIP-DYWYETSFLLWANSVAVNPVLYPLCHYSFRRAFTKLLC 345  
377 VTK 379  
346 PQK 348

RESULT 11  
US-09-165-543-32  
; Sequence 32, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 362 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-165-543-32  
Query Match 28.4%; Score 582.5; DB 3; Length 362;  
Best Local Similarity 37.7%; Pred. No. 1.3e-40;  
Matches 137; Conservative 45; Mismatches 118; Indels 63; Gaps 10;  
65 GLISIPLYIPHVLF-NWNFGSGICMFWLITDYLCTASVYNVILISYDRYQSVNAVSYR 123

Query Match	20.8%;	Score 427;	DB 1;	Length 348;
Best Local Similarity	27.9%;	Pred. No. 9.1e-28;		
Matches 109;	Conservative 76;	Mismatches 119;	Indels 86;	Gaps 12;
QY	16	VPLAFLMSSFAFAVMGNNAVILAFVVDRLNLRHRSNFNFNLALSDFVLGLISLPIPLXPH	75	
Db	2	ITIAVTVAVSLMTIVGNVLVMISFKVNSQLKTVNNYLLSIACADLIIGIFSNNLTTY	61	
QY	76	VLP--NNFSGGICMFMLITDYLLCTASVNNVLISDRYQSVNVSQAQHT----	GI 129	
Db	62	ILIMGRWALGSLACDLWLAIIDYVNASNLMLLVISPDYVFSITRPLTRYAKRTPKRAGI	121	
QY	130	MKIVAQMVAVMILAFVLNGPMILASDW----	KNSTNTKDCBPGFVTEWVILITIMLLE 184	
Db	122	MIGIA-----WLISFILWAFALC----	WQVLVGRKTVPIDECIQIQFSEPTITFGTAIAA 173	
QY	185	FLIPVTSVAYENVQIYMSLWKR-----	RALRCPSPSHAGFSTTSSSASGHLH 230	
Db	174	FYIPVSIIMRILYCRIVRETEKRTKDLADLOGSDSVYKAEKKVAHRA-----	LF 222	
QY	231	RAGVACETSNPGLKESNAASHSPRSRKSSILVSLRTHMNSSITAFKVGSGFWSESAALR	290	
Db	223	RSCLRCPRPTKGLNPSPS--HQMTKKRMS-----	250	
QY	291	QREYAEILLRGRKLARSAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYSIAFWLOW	350	
Db	251	-----LVKERKAQTLISALLAFITWTYTNIMLV-STFCDCKCPVLIWH-LGIWLCTY	302	
QY	351	FNSEVNPFLYPLCHRRPQKAFWKILCVTKW	380	
Db	303	INSTVNPICVLCNRTFRKTFIMLLC--RW	330	

RESULT 13  
PCT-US93-08528-13  
; Sequence 13, Application PC/TUS9308528  
; GENERAL INFORMATION:  
; APPLICANT: New York University  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08528  
; FILING DATE: 09-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 348 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

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; MOLECULE TYPE: peptide
PCT-US93-08528-13

Query Match      20.8%; Score 427; DB 5; Length 348;
Best Local Similarity 27.9%; Pred. No. 9,1e-28;
Matches 109; Conservative 76; Mismatches 119; Indels 86; Gaps 12;

QY 16 VPLAFLMSSFAFIMGVNAVIVIAFVVDRLRHSNYFFLNLAISDELVLGIPIYIPH 75
Db 2 ITIAVVTAVVSLMTIVGVNLVIMISFKVNSQLKTVNNYLLSIACADLIIGIFSMNLYTY 61
QY 76 VLPF--NNFSGSGCMFEWLIITDYLLCTASVYNIVLISVDRYQSVNAVSPQAHT---GI 129
Db 62 ILIMGRWALGSLACDLWLADIYVASNASVNLNLVVISFDYFSTIRPLTYRAKETPKRAGI 121
QY 130 MKIVAQMVAVWILAFILVNGEMILASDSW-----KNSTNTKCEPPGFVTEWVILITIMLLE 184
Db 122 MIGIA-----WLISFILWAPAILC---WQYLVKGRTPVDECOQLSEPTITFGTAIAA 173
QY 185 FLIPVISVAVFNQIYVSLWKR-----RALSRCPSHAGFSTTSSSASGHLH 230
Db 174 FYIPVSMIRILYCKIYRETEKRTKDLADLQGSVDVYKAEKKFAHRA-----LF 222
QY 231 RAGVACETSNPGLKESASRHSSESPPRKSSILVSLKTHMNSSITAPKVGSWFWESEAAALR 290
Db 223 RSLCIRCPRTKGLNPMPNS--HQMTRKRWMS-----250
QY 291 QREYAEALLRGRKLARSIALILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFELQW 350
Db 251 -----LVXERKAAQTLISAILAFITWTPIYIMVLV-STFCDDKCVPTLWH-LGYWLVCY 302
QY 351 FNSFVNPFYPLCHRRFPQAFKWLICVTWK 380
Db 303 INSTVNPICVLCNRTFRKTFIMLLC--RW 330

RESULT 14
US-08-118-270-11
; Sequence 11, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NETMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 11:

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TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-11

Query Match 20.8%; Score 427; DB 5; Length 355;  
Best Local Similarity 29.6%; Pred. No. 9.3e-28;  
Matches 110; Conservative 75; Mismatches 123; Indels 64; Gaps 13;

QY 18 LAFIMSSFAFAMVGNVAVILAFVDRNLHRNRYFFNLAIISDFLVGLISIPLYIPHL 77  
Db 3 IAFETGILAVTIIGNILVIVFKNVKQLKTVNNYFLLSLACADLIIGVISMNLFTTYII 62  
QY 78 FN-WNFGSGICMFWLITDYLLCTASVYVNIIVISYDRYQSVNAVSYRAQHT----GIMKI 132  
Db 63 MNRWALGNTACDLWIAIDYVNASVNLNLLVISDFRYFSITRPLTYRAKRTTKRAGVMIG 122  
QY 133 VAQWAVWILAFVNGPMILASDSKNSNTKCEPG-----FVTEWVILITMLLEFLL 187  
Db 123 LA-----WVISFVLWAPAIL---FWQYFVGKRTVPPGECFIQFUSEPTITFGTAIAAFYM 174  
QY 188 PVISVAYFNVQIYWSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN----PGL 243  
Db 175 PVIMRI-----LYWRIYKETE-KTKELAG-----LQASGTEAETENFVHPTGS 218  
QY 244 KESAASHSPRRKSSILVSLRTHMNSSITAFKVGFWRSSESAALQREYAEALLRQKL 303  
Db 219 SRSCSSVELQOKR-----FALKT--RSQITKRKL-----LVKEKKA 253  
QY 304 ARSLAILLSAFAICWADYCLFTIVLSTYPRTERPKSVWYSTAFLOWNSFVNPFLYPLC 363  
Db 254 AQTLSAILLAFIITWTPTNIMVLV-NTFCDSICPTKYNNLGGYWLVCYNSTVNPVCVYALC 312  
QY 364 HRRFOKAFWKIL 375  
Db 313 NKTFRTFKILL 324

Search completed: October 1, 2004, 10:13:27  
Job time : 20 secs

SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-118-270-11

Query Match 20.8%; Score 427; DB 1; Length 355;  
Best Local Similarity 29.6%; Pred. No. 9.3e-28;  
Matches 110; Conservative 75; Mismatches 123; Indels 64; Gaps 13;

QY 18 LAFIMSSFAFAMVGNVAVILAFVDRNLHRNRYFFNLAIISDFLVGLISIPLYIPHL 77  
Db 3 IAFETGILAVTIIGNILVIVFKNVKQLKTVNNYFLLSLACADLIIGVISMNLFTTYII 62  
QY 78 FN-WNFGSGICMFWLITDYLLCTASVYVNIIVISYDRYQSVNAVSYRAQHT----GIMKI 132  
Db 63 MNRWALGNTACDLWIAIDYVNASVNLNLLVISDFRYFSITRPLTYRAKRTTKRAGVMIG 122  
QY 133 VAQWAVWILAFVNGPMILASDSKNSNTKCEPG-----FVTEWVILITMLLEFLL 187  
Db 123 LA-----WVISFVLWAPAIL---FWQYFVGKRTVPPGECFIQFUSEPTITFGTAIAAFYM 174  
QY 188 PVISVAYFNVQIYWSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN----PGL 243  
Db 175 PVIMRI-----LYWRIYKETE-KTKELAG-----LQASGTEAETENFVHPTGS 218  
QY 244 KESAASHSPRRKSSILVSLRTHMNSSITAFKVGFWRSSESAALQREYAEALLRQKL 303  
Db 219 SRSCSSVELQOKR-----FALKT--RSQITKRKL-----LVKEKKA 253  
QY 304 ARSLAILLSAFAICWADYCLFTIVLSTYPRTERPKSVWYSTAFLOWNSFVNPFLYPLC 363  
Db 254 AQTLSAILLAFIITWTPTNIMVLV-NTFCDSICPTKYNNLGGYWLVCYNSTVNPVCVYALC 312  
QY 364 HRRFOKAFWKIL 375  
Db 313 NKTFRTFKILL 324

RESULT 15  
PCT-US93-08528-11  
Sequence 11, Application PC/TUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:11:54 ; Search time 134 Seconds  
(without alignments)

938.981 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSENSTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1370.5	66.9	390	9	US-09-910-411-2
2	1370.5	66.9	390	10	US-09-852-165-2
3	1370.5	66.9	390	10	US-09-891-138A-6
4	1370.5	66.9	390	12	US-10-349-253A-2
5	1370.5	66.9	390	12	US-09-875-076-14
6	1370.5	66.9	390	12	US-09-876-252-14
7	1370.5	66.9	390	13	US-10-052-193-2
8	1370.5	66.9	390	14	US-10-225-567A-629
9	1370.5	66.9	390	14	US-10-272-983-14
10	1370.5	66.9	390	14	US-10-354-769-2
11	1370.5	66.9	390	14	US-10-393-807-14
12	1370.5	66.9	390	15	US-10-417-820A-14
13	1370.5	66.9	390	16	US-10-696-673-2
14	1370.5	66.9	390	16	US-10-723-955-14
15	1370.5	66.9	390	16	US-10-737-619-2

16	1370.5	66.9	390	16	US-10-782-596-14	Sequence 14, Appl
17	1366.5	66.7	390	14	US-10-290-078-27	Sequence 27, Appl
18	722.5	35.3	445	9	US-09-350-206-2	Sequence 2, Appl
19	722.5	35.3	445	9	US-09-349-755-2	Sequence 2, Appl
20	722.5	35.3	445	9	US-09-166-334-2	Sequence 2, Appl
21	722.5	35.3	445	14	US-10-282-958-2	Sequence 2, Appl
22	722.5	35.3	445	14	US-10-225-567A-549	Sequence 549, App
23	722.5	35.3	445	16	US-10-453-106-1	Sequence 1, Appl
24	722.5	35.3	445	16	US-10-727-021-7	Sequence 7, Appl
25	722.5	35.3	445	12	US-09-891-053-20	Sequence 20, Appl
26	718.5	35.1	445	16	US-10-453-106-2	Sequence 2, Appl
27	716.5	35.0	445	9	US-09-350-206-5	Sequence 5, Appl
28	716.5	35.0	445	9	US-09-349-755-5	Sequence 5, Appl
29	716.5	35.0	445	9	US-09-166-334-5	Sequence 25, Appl
30	716.5	35.0	445	12	US-09-891-053-25	Sequence 5, Appl
31	716.5	35.0	445	14	US-10-282-958-5	Sequence 3, Appl
32	716.5	35.0	445	16	US-10-453-106-3	Sequence 1, Appl
33	709.5	34.6	413	12	US-09-891-053-1	Sequence 3, Appl
34	591	28.9	441	16	US-10-398-036-3	Sequence 32, Appl
35	582.5	28.4	362	9	US-09-350-206-32	Sequence 188, App
36	582.5	28.4	362	9	US-09-349-755-32	Sequence 10, Appl
37	582.5	28.4	362	9	US-09-166-334-32	Sequence 22, Appl
38	582.5	28.4	362	14	US-10-282-958-32	Sequence 82, Appl
39	413	20.2	460	14	US-10-225-567A-188	Sequence 6, Appl
40	413	20.2	478	13	US-10-029-009-10	Sequence 93, Appl
41	413	20.2	498	13	US-10-029-009-22	Sequence 6, Appl
42	410	20.0	460	9	US-09-782-980-82	Sequence 3, Appl
43	410	20.0	460	9	US-09-884-430-6	Sequence 32, Appl
44	410	20.0	460	12	US-10-423-543-93	Sequence 32, Appl
45	410	20.0	460	14	US-10-336-489-6	Sequence 32, Appl

#### ALIGNMENTS

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RESULT 1
US-09-910-411-2
; Sequence 2, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-910-411-2

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Query Match 66.9%; Score 1370.5; DB 9; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy 1 MSENSTGILPPAAQVPLAFMSFAIMVGNVILAFVVDNRNLRHSYFFFLNLAIS 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MPDNTNINSLSTRVTLAFPMFLVAFALGNALVILAFVVDNRNLRHSYFFFLNLAIS 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 61 DELVGLSIPLYIPIHVLENFNWFGSGICMFNWLITDYLCTASVYNIIVLSYDRYOSVNAV 120
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 61 DFFVGVISIPLYIPHTLFEWDFQKEICVFWLTDYLLCTASVYVNIIVLSYDRYLSVSNV 120  
QY 121 SYRAQHTGIMKIVAOVAVWVILAFVNGPMILASDWNKSTNTKDCPFGVTEWYILIT 180  
Db 121 SYRTQHTGVKIVTLVAVWVILAFVNGPMILASDWNKSTNTKDCPFGVTEWYILIT 178  
QY 181 MLEFLLPVISVAYFNVQIYVWLSWKRRALSRCPHAGFTSTSSASGHLHRAVACRTSN 240  
Db 179 SFLEFVPIVILVAYFNNIYVWLSWKRRALSRCPHAGFTSTSSASGHLHRAVACRTSN 238  
QY 241 PGLKESAAHSHSPRRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEILRG 300  
Db 239 SASTEVPAHSHRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVLHQREHVELLRA 298  
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360  
Db 299 RRLAKSLAILLGFAVCAWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPLY 358  
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391  
Db 359 PLCHKEFQKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 2

US-09-852-165-2  
; Sequence 2, Application US/09852165  
; Publication No. US20030032784A1  
; GENERAL INFORMATION:  
; APPLICANT: Lind, Peter  
; APPLICANT: Sejlitz, Torsten  
; APPLICANT: Vogeli, Gabriel  
; TITLE OF INVENTION: No. US20030032784A1 G Protein-Coupled Receptors  
; FILE REFERENCE: 00231regUS  
; CURRENT APPLICATION NUMBER: US/09/852,165  
; CURRENT FILING DATE: 2001-05-08  
; PRIOR FILING DATE: USN 60/203,108  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 2  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-852-165-2

Query Match 66.9%; Score 1370.5; DB 10; Length 390;  
Best Local Similarity 68.1%; Pred. No. 3.2e-119;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
QY 1 MSESNTGILPPAAQVPLAFMSSPFAIMVGNVAVILAFVVDNRHRSNYFFLNLAIS 60  
Db 1 MPDNTNSTINLSLSTRVTLAFFMSLVAFALMGNALVILAFVVDNRHRSNYFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPHTLFEWDFQKEICVFWLTDYLLCTASVYVNIIVLSYDRYLSVSNV 120  
Db 61 DFFVGVISIPLYIPHTLFEWDFQKEICVFWLTDYLLCTASVYVNIIVLSYDRYLSVSNV 120  
QY 121 SYRAQHTGIMKIVAOVAVWVILAFVNGPMILASDWNKSTNTKDCPFGVTEWYILIT 180  
Db 121 SYRTQHTGVKIVTLVAVWVILAFVNGPMILASDWNKSTNTKDCPFGVTEWYILIT 178  
QY 181 MLEFLLPVISVAYFNVQIYVWLSWKRRALSRCPHAGFTSTSSASGHLHRAVACRTSN 240  
Db 179 SFLEFVPIVILVAYFNNIYVWLSWKRRALSRCPHAGFTSTSSASGHLHRAVACRTSN 238  
QY 241 PGLKESAAHSHSPRRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEILRG 300  
Db 239 SASTEVPAHSHRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVLHQREHVELLRA 298  
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360  
Db 299 RRLAKSLAILLGFAVCAWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPLY 358

QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391  
Db 359 PLCHKEFQKAFKIFCIKQPLPSQHSRSVSS 390  
RESULT 3  
US-09-891-138A-6  
; Sequence 6, Application US/09891138A  
; Publication No. US20030083245A1  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Daniel Chi-Hong  
; APPLICANT: Zhao, Jiagang  
; APPLICANT: Chen, Jin-Long  
; APPLICANT: Cutler, Gene  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: No. US20030083245A1alel Receptors  
; FILE REFERENCE: 018781-006210US  
; CURRENT APPLICATION NUMBER: US/09/891,138A  
; CURRENT FILING DATE: 2001-06-25  
; PRIOR FILING DATE: US 60/213,461  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patent in ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)  
US-09-891-138A-6

Query Match 66.9%; Score 1370.5; DB 10; Length 390;  
Best Local Similarity 68.1%; Pred. No. 3.2e-119;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
QY 1 MSESNTGILPPAAQVPLAFMSSPFAIMVGNVAVILAFVVDNRHRSNYFFLNLAIS 60  
Db 1 MPDNTNSTINLSLSTRVTLAFFMSLVAFALMGNALVILAFVVDNRHRSNYFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPHTLFEWDFQKEICVFWLTDYLLCTASVYVNIIVLSYDRYLSVSNV 120  
Db 61 DFFVGVISIPLYIPHTLFEWDFQKEICVFWLTDYLLCTASVYVNIIVLSYDRYLSVSNV 120  
QY 121 SYRAQHTGIMKIVAOVAVWVILAFVNGPMILASDWNKSTNTKDCPFGVTEWYILIT 180  
Db 121 SYRTQHTGVKIVTLVAVWVILAFVNGPMILASDWNKSTNTKDCPFGVTEWYILIT 178  
QY 181 MLEFLLPVISVAYFNVQIYVWLSWKRRALSRCPHAGFTSTSSASGHLHRAVACRTSN 240  
Db 179 SFLEFVPIVILVAYFNNIYVWLSWKRRALSRCPHAGFTSTSSASGHLHRAVACRTSN 238  
QY 241 PGLKESAAHSHSPRRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEILRG 300  
Db 239 SASTEVPAHSHRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVLHQREHVELLRA 298  
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360  
Db 299 RRLAKSLAILLGFAVCAWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPLY 358  
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391  
Db 359 PLCHKEFQKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 4

US-10-349-253A-2  
; Sequence 2, Application US/10349253A  
; Publication No. US20040043393A1  
; GENERAL INFORMATION:  
; APPLICANT: Aubart, Kelly  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Fitzgerald, Laura

APPLICANT: Graybill, Todd  
APPLICANT: Li, Xiatong  
APPLICANT: Michalovich, David  
APPLICANT: Morrow, Dwight  
APPLICANT: Zhu, Yuan

TITLE OF INVENTION: AKOR35, A G-Protein Coupled Receptor

CURRENT APPLICATION NUMBER: US/10/349,253A

PRIOR FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: 09/910,411

PRIOR FILING DATE: 2001-07-20

PRIOR APPLICATION NUMBER: 09/693,761

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 09/497,790

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/431,898

PRIOR FILING DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 390

TYPE: PRT

ORGANISM: Homo sapien

US-10-349-253A-2

Query Match 66.9%; Score 1370.5; DB 12; Length 390;  
Best Local Similarity 68.1%; Pred. No. 3.2e-119;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMSSFAFALMVGNVILAFVVDNRNLHRSNYFFNLALIS 60  
DB 1 MPTNTSTNLSTRTVTLAFMSLVAFALMGNALVILAFVVDKRLHRSNYFFNLALIS 60  
QY 61 DFLVGLISIPYIPHLFNNFNGSGICMFWLITDYLLCTASVYVNIIVLSYDRYQSVNAV 120  
DB 61 DPFVGVISIPYIPHLFNNFNGSGICMFWLITDYLLCTASVYVNIIVLSYDRYQSVNAV 120  
QY 121 SYRQHTGIMKIVQAVVAVVILAFVNGPMLASDSWKNSTNTKDCPEGFVTEWYILAIT 180  
DB 121 SYRQHTGIMKIVQAVVAVVILAFVNGPMLASDSWKNSTNTKDCPEGFVTEWYILAIT 180  
QY 181 MLLEFLLPVISVAVFNVQIYWSLWKRRLSRCPHAGFSTSSASGHLHRAVACRTSN 240  
DB 179 SFLEFVIVPILVAFNNIYWSLWKRDLHRCQHPGLTAVSSNICCHSPRGLSRSL 238  
QY 241 PGLKESAAHRHSEPRKSSILVLRTHMNSSITAFKVGSEFWSAESALRQREYAEILRG 300  
DB 239 SASTEVPAFHSERQRRKSSLMFSSRTKMSNTIASKMGFSQSDSVLHREHVELLRA 298  
QY 301 RKLARSALLLSAFACWAPYCLFTIVLSTYRTERPKSVKYSIAFWLQWNSFVNPLY 360  
DB 299 RRLAKSLALLGVAVCAWAPYSLFTIVLSTYRTERPKSVKYSIAFWLQWNSFVNPLY 358  
QY 361 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 391  
DB 359 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 390

## RESULT 5

US-09-875-076-14  
Sequence 14, Application US/09875076  
Publication No. US20030017528A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Ruoping  
APPLICANT: Dang, Huang T.  
APPLICANT: Liaw, Chen W.  
APPLICANT: Lin, I-Lin  
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
FILE REFERENCE: AREN0050  
CURRENT APPLICATION NUMBER: US/09/875,076  
CURRENT FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 09/417,044  
PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 60/120,416  
PRIOR FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: 60/121,851  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/123,946  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,949  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/136,436  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,437  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,439  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,567  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/137,127  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/137,131  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/141,448  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 60/156,653  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,633  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,555  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,634  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/157,280  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,294  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,281  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,293  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,282  
PRIOR FILING DATE: 1999-10-01  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 390  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-875-076-14

Query Match 66.9%; Score 1370.5; DB 12; Length 390;  
Best Local Similarity 68.1%; Pred. No. 3.2e-119;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMSSFAFALMVGNVILAFVVDNRNLHRSNYFFNLALIS 60  
DB 1 MPTNTSTNLSTRTVTLAFMSLVAFALMGNALVILAFVVDKRLHRSNYFFNLALIS 60  
QY 61 DFLVGLISIPYIPHLFNNFNGSGICMFWLITDYLLCTASVYVNIIVLSYDRYQSVNAV 120  
DB 61 DPFVGVISIPYIPHLFNNFNGSGICMFWLITDYLLCTASVYVNIIVLSYDRYQSVNAV 120  
QY 121 SYRQHTGIMKIVQAVVAVVILAFVNGPMLASDSWKNSTNTKDCPEGFVTEWYILAIT 180  
DB 121 SYRQHTGIMKIVQAVVAVVILAFVNGPMLASDSWKNSTNTKDCPEGFVTEWYILAIT 180  
QY 181 MLLEFLLPVISVAVFNVQIYWSLWKRRLSRCPHAGFSTSSASGHLHRAVACRTSN 240  
DB 179 SFLEFVIVPILVAFNNIYWSLWKRDLHRCQHPGLTAVSSNICCHSPRGLSRSL 238  
QY 241 PGLKESAAHRHSEPRKSSILVLRTHMNSSITAFKVGSEFWSAESALRQREYAEILRG 300  
DB 239 SASTEVPAFHSERQRRKSSLMFSSRTKMSNTIASKMGFSQSDSVLHREHVELLRA 298  
QY 301 RKLARSALLLSAFACWAPYCLFTIVLSTYRTERPKSVKYSIAFWLQWNSFVNPLY 360

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Db      299 RRLAKSLAILGVFVAVCWAPYSLFTVLVSFYSSATGPKSVWYRIAFWLQWNSFVNPLLY 358
QY      361 PLCHRRFOKAFWKILCVTKWPALSQ-NQSVSS 391
Db      359 PLCHRRFOKAFKIKFCIKKQPLPSQHSRSVSS 390

RESULT 6
US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29

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Query Match 66.9%; Score 1370.5; DB 13; Length 390;  
Best Local Similarity 68.1%; Pred. No. 3.2e-119;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNLRHRSYFFFLNLAIS 60  
DB 1 MPDNTNINLSLSTRVTLAFMGLVAFVVDNLRHRSYFFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVILSYDRYQSVNAV 120  
DB 61 DFFVGVISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVILSYDRYQSVNAV 120  
QY 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMTILASDSWKNSNTKDCBPGFVTEWILIT 180  
DB 121 SYRTOHTGVKIVLWVAVVILAFVNGPMTILVSESWKDEGS--ECBPGFSEWILAIT 178  
QY 181 MLLEFLLPVISVAYFNVOIYWSLWKRRLSRCPHAGFSTTSSASGHLHRAGVACRTSN 240  
DB 179 SFLEFVPIVLVAYFNWNIYWSLWKRDLHRCQHPGLTAVSSNICGHSFRGLSSRRSL 238  
QY 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGSPWRSESAAALROREYAEILRG 300  
DB 239 SASTEVPAFSPHSEQRKSSILMFSSRTKMSNTTASXWGSFQSDSVLHOREHVELLRA 298  
QY 301 RKLARSIAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYIAFWLQWNSFVNPLY 360  
DB 299 RRLAKSLAILLGVAVCAWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPLY 358  
QY 361 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 391  
DB 359 PLCHKRFQKAFKLFCKIKQPLFSQHSRSVSS 390

RESULT 8  
US-10-225-567A-629  
; Sequence 629, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 629  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-629

Query Match 66.9%; Score 1370.5; DB 14; Length 390;  
Best Local Similarity 68.1%; Pred. No. 3.2e-119;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNLRHRSYFFFLNLAIS 60  
DB 1 MPDNTNINLSLSTRVTLAFMGLVAFVVDNLRHRSYFFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVILSYDRYQSVNAV 120  
DB 61 DFFVGVISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVILSYDRYQSVNAV 120  
QY 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMTILASDSWKNSNTKDCBPGFVTEWILIT 180  
DB 121 SYRTOHTGVKIVLWVAVVILAFVNGPMTILVSESWKDEGS--ECBPGFSEWILAIT 178  
QY 181 MLLEFLLPVISVAYFNVOIYWSLWKRRLSRCPHAGFSTTSSASGHLHRAGVACRTSN 240

DB 179 SFLEFVPIVLVAYFNWNIYWSLWKRDLHRCQHPGLTAVSSNICGHSFRGLSSRRSL 238  
QY 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGSPWRSESAAALROREYAEILRG 300  
DB 239 SASTEVPAFSPHSEQRKSSILMFSSRTKMSNTTASXWGSFQSDSVLHOREHVELLRA 298  
QY 301 RKLARSIAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYIAFWLQWNSFVNPLY 360  
DB 299 RRLAKSLAILLGVAVCAWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPLY 358  
QY 361 PLCHRRFQKAFWKILCVTKWPAISO-NQSVSS 391  
DB 359 PLCHKRFQKAFKLFCKIKQPLFSQHSRSVSS 390

RESULT 9  
US-10-272-983-14  
; Sequence 14, Application US/10272983  
; Publication No. US20030148450A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/272,983  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-272-983-14

Query Match 66.9%; Score 1370.5; DB 14; Length 390;  
Best Local Similarity 68.1%; Pred. No. 3.2e-119;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSENSTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNLRHRSYFFFLNLAIS 60  
DB 1 MPDNTNINLSLSTRVTLAFMGLVAFVVDNLRHRSYFFFLNLAIS 60  
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVILSYDRYQSVNAV 120  
DB 61 DFFVGVISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNVILSYDRYQSVNAV 120  
QY 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMTILASDSWKNSNTKDCBPGFVTEWILIT 180  
DB 121 SYRTOHTGVKIVLWVAVVILAFVNGPMTILVSESWKDEGS--ECBPGFSEWILAIT 178

QY 181 MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACTSN 240  
Db 179 SFLEFVPIVLVAYFNNIYWSLWKRDHLSCQSHFGLTAVSSNICHSFGRSLSRRL 238  
QY 241 PGLKESAAHSHSPRRKSSILVSLRTHMNSSITAFKVGFSFMRSESAALRQREYAEILRG 300  
Db 239 SASTEPVAPSHSRQRKSSLMFSSRTKMNNTIASKMGFSQSDSVLHQREHVELLRA 298  
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPTERPKSVYVIAFWLQWNSFVNPFLLY 360  
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVYVIAFWLQWNSFVNPFLLY 358  
QY 361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391  
Db 359 PLCHKRFQKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 10  
US-10-354-769-2  
; Sequence 2, Application US/10354769  
; Publication No. US20030149242A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: O'Reilly, Mark A.  
; APPLICANT: Peter, Beate  
; TITLE OF INVENTION: NOVEL POLYPEPTIDE  
; FILE REFERENCE: PC10373B  
; CURRENT APPLICATION NUMBER: US/10354,769  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US 09/598,801  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/211,243  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: GB 9925641.4  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: GB 0009973.9  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-354-769-2

Query Match 66.9%; Score 1370.5; DB 14; Length 390;  
Best Local Similarity 68.1%; Pred. No. 3.2e-119;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFALMGVNAVILAFVVDRLNRHRSNYFFNLALS 60  
Db 1 MPDNTNINLSLSTRVTLAFFMSLVAFALMGNALVILAFVVDKRLRHSSYFFNLALS 60  
QY 61 DFLVGLISLPIYPIPHVLFNWFGSGICMFWLITDYLLCTASVNIIVLSIDRYQSVSNV 120  
Db 61 DFFVGVISIPIYPIHPLFDWDFGKEICVFMTDYLCTASVNIIVLSIDRYLSVSNV 120  
QY 121 SYRAQHTGMKIVQAVQVAVMILAFVNGPMLASDSWKNTNTKCEPGFVTEWYILIT 180  
Db 121 SYRTQHTGVKIVLTMVAVVAVLAFVNGPMLIVSVESWKDEGS--ECEPGFFSEWYILAIT 178  
QY 181 MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACTSN 240  
Db 179 SFLEFVPIVLVAYFNNIYWSLWKRDHLSCQSHFGLTAVSSNICHSFGRSLSRRL 238  
QY 241 PGLKESAAHSHSPRRKSSILVSLRTHMNSSITAFKVGFSFMRSESAALRQREYAEILRG 300  
Db 239 SASTEPVAPSHSRQRKSSLMFSSRTKMNNTIASKMGFSQSDSVLHQREHVELLRA 298  
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPTERPKSVYVIAFWLQWNSFVNPFLLY 360  
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVYVIAFWLQWNSFVNPFLLY 358

QY 361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391  
Db 359 PLCHKRFQKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 11  
US-10-393-807-14  
; Sequence 14, Application US/10393807  
; Publication No. US20030175891A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/393,807  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-393-807-14

Query Match 66.9%; Score 1370.5; DB 14; Length 390;  
Best Local Similarity 68.1%; Pred. No. 3.2e-119;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFALMGVNAVILAFVVDRLNRHRSNYFFNLALS 60  
Db 1 MPDNTNINLSLSTRVTLAFFMSLVAFALMGNALVILAFVVDKRLRHSSYFFNLALS 60  
QY 61 DFLVGLISLPIYPIPHVLFNWFGSGICMFWLITDYLLCTASVNIIVLSIDRYQSVSNV 120  
Db 61 DFFVGVISIPIYPIHPLFDWDFGKEICVFMTDYLCTASVNIIVLSIDRYLSVSNV 120  
QY 121 SYRAQHTGMKIVQAVQVAVMILAFVNGPMLASDSWKNTNTKCEPGFVTEWYILIT 180  
Db 121 SYRTQHTGVKIVLTMVAVVAVLAFVNGPMLIVSVESWKDEGS--ECEPGFFSEWYILAIT 178  
QY 181 MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACTSN 240  
Db 179 SFLEFVPIVLVAYFNNIYWSLWKRDHLSCQSHFGLTAVSSNICHSFGRSLSRRL 238  
QY 241 PGLKESAAHSHSPRRKSSILVSLRTHMNSSITAFKVGFSFMRSESAALRQREYAEILRG 300  
Db 239 SASTEPVAPSHSRQRKSSLMFSSRTKMNNTIASKMGFSQSDSVLHQREHVELLRA 298  
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPTERPKSVYVIAFWLQWNSFVNPFLLY 360

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Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRTAFWQLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 391
Db 359 PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 390

RESULT 12
US-10-417-820A-14
; Sequence 14, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR FILING DATE: 09/416,760
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-820A-14

Query Match 66.9%; Score 1370.5; DB 15; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFALMGNVAVILAFVVDNRNHRSNFYFNLNLAIS 60
Db 1 MPDTNSTINLSLSTRVTLTAFFMSLVAFALMGNALVILAFVVDNKNLRHRSYFNLNLAIS 60
QY 61 DFLVGLISIPLYIPHVLFWNFSGICMPFLITDYLLCTASVYNIIVLISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTIDYLLCTASVYNIIVLISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIYAQWAVVILAFVNGPMILASDWSKNSTNTKDCPGFVTEWILIT 180
Db 121 SYRTQHTGVLKIVLMAVAVVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWILAIT 178
QY 181 MLLEFLLPVISVAYVNVQIYSLWKRRALSRCPHAGFTSSSSAGSHLHRAGVACRTSN 240
Db 179 SFLEFVIPVILVAYVNMNIYSLWKRDHLRCQSPHGLTAVSSNCGHSFGRGSSRSL 238
QY 241 PGLKESAAHSRSESPPRKSSILVSLRTHMNSSITAFKVGSWRSESAAALRQREYAEILRG 300
Db 239 SASTEVPASFHSEQRKRKSLMFSSRTKNSNTIASKMGFSQSDSVVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRTAFWQLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 391
Db 359 PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 390

RESULT 14
US-10-723-955-14
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QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRTAFWQLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 391
Db 359 PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 390

RESULT 13
US-10-696-673-2
; Sequence 2, Application US/10696673
; Publication No. US20040105846A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogel, Gabriel
; APPLICANT: Wood, Linda S
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: PHRM0025-101/00231REGUS.1 DVI
; CURRENT APPLICATION NUMBER: US/10/696,673
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 60/203,108
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: US 09/852,165
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-696-673-2

Query Match 66.9%; Score 1370.5; DB 16; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFALMGNVAVILAFVVDNRNHRSNFYFNLNLAIS 60
Db 1 MPDTNSTINLSLSTRVTLTAFFMSLVAFALMGNALVILAFVVDNKNLRHRSYFNLNLAIS 60
QY 61 DFLVGLISIPLYIPHVLFWNFSGICMPFLITDYLLCTASVYNIIVLISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTIDYLLCTASVYNIIVLISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIYAQWAVVILAFVNGPMILASDWSKNSTNTKDCPGFVTEWILIT 180
Db 121 SYRTQHTGVLKIVLMAVAVVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWILAIT 178
QY 181 MLLEFLLPVISVAYVNVQIYSLWKRRALSRCPHAGFTSSSSAGSHLHRAGVACRTSN 240
Db 179 SFLEFVIPVILVAYVNMNIYSLWKRDHLRCQSPHGLTAVSSNCGHSFGRGSSRSL 238
QY 241 PGLKESAAHSRSESPPRKSSILVSLRTHMNSSITAFKVGSWRSESAAALRQREYAEILRG 300
Db 239 SASTEVPASFHSEQRKRKSLMFSSRTKNSNTIASKMGFSQSDSVVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRTAFWQLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 391
Db 359 PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 390

RESULT 14
US-10-723-955-14
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358

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Sequence 14, Application US/10723955
Publication No. US20040110238A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lin, I-Lin
APPLICANT: Liaw, Chen W.
APPLICANT: Lehman-Bruinsma, Karin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Gore, Martin
APPLICANT: White, Carol
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
Receptors
FILE REFERENCE: 7. US29.CON
CURRENT APPLICATION NUMBER: US/10723,955
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 10/417,820
PRIOR FILING DATE: 2003-4-16
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-955-14

Query Match 66.9%; Score 1370.5; DB 16; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNLRHRSYFFNLALS 60
Db 1 MPDNTNLSLSTRVTLAFMSLVAFALMGNALVILAFVVDNLRHRSYFFNLALS 60
QY 61 DFLVGLISIPLYIPHLFNNWFGSGICMFWLITDYLLCTASVYNIIVLISYDRYSVNAV 120
Db 61 DFLVGLISIPLYIPHLFNNWFGSGICMFWLITDYLLCTASVYNIIVLISYDRYSVNAV 120
QY 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFVWLTDDYLLCTASVYNIIVLISYDRYSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFVWLTDDYLLCTASVYNIIVLISYDRYSVNAV 120
QY 121 SYRAQHTGIMKIVQAVMVAWVILAFVNGPMILASDSWKNSTNTKDCPGFVTEWYILIT 180
Db 121 SYRTQHTGVKIVLTVLMAVWVILAFVNGPMILVSVESWKNDEGS--ECEPGFFSEWYILAIT 178
QY 181 MLEFLLEPVISVAYFNVOIYWSLWKRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SPLEFVIPVILVAYFNNNIYWSLWKRDLHLSRCQSHPLGTAVSSNTCGHSFGRLSRRSL 238
QY 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSSITAFKVGFSWRSESAALRQREYAEALLRG 300
Db 239 SASTEVPAPSHSERQRRKSSLMFSSRTKMNSTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVYVYSIAFWLQWNSFVNPLY 360
Db 179 SPLEFVIPVILVAYFNNNIYWSLWKRDLHLSRCQSHPLGTAVSSNTCGHSFGRLSRRSL 238
QY 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSSITAFKVGFSWRSESAALRQREYAEALLRG 300
Db 239 SASTEVPAPSHSERQRRKSSLMFSSRTKMNSTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVYVYSIAFWLQWNSFVNPLY 360
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Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
Db 359 PLCHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 15
US-10-737-619-2
Sequence 2, Application US/10737619
Publication No. US20040138234A1
GENERAL INFORMATION:
APPLICANT: Pfizer, Inc.
TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
FILE REFERENCE: PC10963A
CURRENT APPLICATION NUMBER: US/10737,619
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: 0101223.6
PRIOR FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-737-619-2

Query Match 66.9%; Score 1370.5; DB 16; Length 390;
Best Local Similarity 68.1%; Pred. No. 3.2e-119;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNLRHRSYFFNLALS 60
Db 1 MPDNTNLSLSTRVTLAFMSLVAFALMGNALVILAFVVDNLRHRSYFFNLALS 60
QY 61 DFLVGLISIPLYIPHLFNNWFGSGICMFWLITDYLLCTASVYNIIVLISYDRYSVNAV 120
Db 61 DFLVGLISIPLYIPHLFNNWFGSGICMFWLITDYLLCTASVYNIIVLISYDRYSVNAV 120
QY 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFVWLTDDYLLCTASVYNIIVLISYDRYSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFVWLTDDYLLCTASVYNIIVLISYDRYSVNAV 120
QY 121 SYRAQHTGIMKIVQAVMVAWVILAFVNGPMILASDSWKNSTNTKDCPGFVTEWYILIT 180
Db 121 SYRTQHTGVKIVLTVLMAVWVILAFVNGPMILVSVESWKNDEGS--ECEPGFFSEWYILAIT 178
QY 181 MLEFLLEPVISVAYFNVOIYWSLWKRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SPLEFVIPVILVAYFNNNIYWSLWKRDLHLSRCQSHPLGTAVSSNTCGHSFGRLSRRSL 238
QY 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSSITAFKVGFSWRSESAALRQREYAEALLRG 300
Db 239 SASTEVPAPSHSERQRRKSSLMFSSRTKMNSTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVYVYSIAFWLQWNSFVNPLY 360
Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
Db 359 PLCHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390
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Search completed: October 1, 2004, 10:22:50  
Job time : 136 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 1, 2004, 10:07:13 ; Search time 18 Seconds  
(without alignments)  
2089.494 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78.\*

2: PIR1.\*

3: PIR2.\*

4: PIR3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1370.5	66.9	390	2 JC7566	histamine H4 recep
2	413	20.2	460	2 A24325	muscarinic acetyl
3	413	20.2	460	2 S09508	muscarinic acetyl
4	410.5	20.0	531	2 JT0531	muscarinic acetyl
5	410.5	20.0	590	2 S01114	muscarinic acetyl
6	410	20.0	460	2 A29514	muscarinic acetyl
7	410	20.0	460	2 IS1837	muscarinic recep
8	409.5	20.0	590	2 S47572	muscarinic acetyl
9	403	19.7	589	2 A29476	muscarinic acetyl
10	402.5	19.7	590	2 S10128	muscarinic acetyl
11	402	19.6	589	2 B29519	muscarinic acetyl
12	401	19.6	639	2 A55019	muscarinic acetyl
13	400	19.5	460	2 A31897	muscarinic acetyl
14	399.5	19.5	532	2 JT0530	muscarinic acetyl
15	392.5	19.2	477	2 S71323	muscarinic acetyl
16	392	19.1	490	2 A35446	alpha-1A adrenerg
17	390.5	19.1	400	2 G00013	muscarinic acetyl
18	390.5	19.1	501	2 JH0447	D3 dopamine recep
19	389.5	19.0	400	2 G01977	alpha-1A-adrenerg
20	389.5	19.0	515	2 A40491	d3 dopamine recep
21	388.5	19.0	491	2 A41632	alpha-1-adrenerg
22	388.5	19.0	572	2 I39369	histamine H1 recep
23	386.5	18.9	487	2 JC2495	alpha-1A-adrenerg
24	385.5	18.8	488	2 I56507	histamine H1 recep
25	384.5	18.8	517	2 A45121	histamine H1 recep
26	382.5	18.7	560	2 A38731	alpha-1B adrenerg
27	382	18.7	479	2 S10127	alpha-1A adrenerg
28	380.5	18.6	466	2 S10126	muscarinic acetyl
29	380.5	18.6	501	2 T18863	hypothetical prote

30	380	18.6	432	2 I50829	alpha 2-adrenocept
31	380	18.6	466	2 A40972	muscarinic acetyl
32	379.5	18.5	466	2 JH0197	muscarinic acetyl
33	379.5	18.5	466	2 S10856	muscarinic acetyl
34	379.5	18.5	515	2 JC1525	alpha-1B-adrenerg
35	379	18.5	486	2 JC1415	histamine H1 recep
36	377.5	18.4	379	2 JC6178	serotonin recep
37	376	18.4	478	2 C29514	muscarinic acetyl
38	374.5	18.3	479	2 S33776	muscarinic acetyl
39	369.5	18.0	466	2 A27386	muscarinic acetyl
40	367.5	17.9	366	2 A47321	serotonin recep
41	367	17.9	484	2 S48657	muscarinic acetyl
42	366.5	17.9	484	2 S58868	G protein-coupled
43	366	17.9	466	2 A35375	alpha-1-adrenerg
44	364.5	17.8	366	2 A47385	serotonin recep
45	360.5	17.6	365	2 S26048	serotonin recep

## ALIGNMENTS

### RESULT 1

JC7566

histamine H4 receptor, HH4R - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001

C;Accession: JC7566

R;Nakamura, T.; Itadani, H.; Hidak, Y.; Ohta, M.; Tanaka, K.

A;Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.

A;Reference number: JC7566; MUID: 20568725; PMID:11118334

A;Contents: Leukocyte

A;Accession: JC7566

A;Molecule type: mRNA

A;Residues: 1-390 <NAK>

A;Cross-references: DDBJ:AB045370

C;Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled

C;Genetics:

A;Gene: hh4r

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match	66.9%;	Score	1370.5;	DB 2;	Length	390;			
Best Local Similarity	68.1%;	Pred. No.	4.3e-110;						
Matches	267;	Conservative	40;	Mismatches	82;	Indels	3;	Gaps	2;
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Db	1	MPDTNSTINLSLSTRVTLAF	MSLVAFALMGNALVILAFVVDKLRHRSNYFFFLNLAI	60					
QY	61	DFVLGLISIPLYIPHLVFN	WFGSGICMPFLITDYLCTASVYNTVLISYDRYQSVSNV	120					
Db	61	DFVGVISIPLYIPHTLPEW	DGKEICVFWLTDTYLLCTASVYNTVLISYDRYLSVSNV	120					
QY	121	SYRAQHTGMKIVAOVAVIL	AFVNGPMILASDWKNSNTKCEPGFVTEWYIT	180					
Db	121	SYRTQHTGVKLIVLWVAV	ILAFVNGPMILVSEWKEGS-ECPEGFSEWYIT	178					
QY	181	MLLEFLLPVISVAYENVQI	YWSLWKRRLSRCPSHAGFTTSSASGHLHRAGVACRTN	240					
Db	179	SFLEFVPIVILVAYNMNI	YWSLWKRDLHRSQSHPGITAVSSNICGHSFGRLLSRSL	238					
QY	241	PLKESASRHSRSPRKS	SLVSLRTHMNSITAFKVGFSFWRSESAALRQREYAEPLRG	300					
Db	239	SASTEVPASFSRQRKSS	LMFSRRTQMNNTIASKMGFSQSDSVLHQREHVELLRA	298					
QY	301	RKLARSAILLSAPAI	WAPYCIETIVLSTPRTERPKSVWYVSTAFMLQWPNFVNPLY	360					
Db	299	RRLAKSAILLGFAV	CWAPYSLFTIIVLSFYSSATGPKSVWYRIAFWLFQWPNFVNPLY	358					
QY	361	PLCHRRFQKAPWKIL	CVTKWPALSQ-NQSVSS	391					
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A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA  
A;Residues: 1-460 <CHA>  
A;Cross-references: EMBL:X52068; NID:g34450; PIDN:CAA36291.1; PID:g34451  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990  
R;Allard, W.J.; Sigal, I.S.; Dixon, R.A.F.  
Nucleic Acids Res. 15, 10604, 1987  
A;Title: Sequence of the gene encoding the human M1 muscarinic acetylcholine receptor.  
A;Reference number: S06327; MUID:88096607; PMID:3697105  
A;Accession: S06327  
A;Molecule type: DNA  
A;Residues: 1-460 <ALL>  
A;Cross-references: GB:Y00508; GB:M35128; NID:g297405; PIDN:CAA68560.1; PID:g297406  
R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of two human muscarinic acetylcholine receptor subtypes.  
A;Reference number: S04326; MUID:88166632; PMID:3443095  
A;Accession: S04326  
A;Molecule type: DNA  
A;Residues: 1-172, 'M', 174-460 <PER>  
A;Cross-references: EMBL:X15263; NID:g32317; PIDN:CAA33334.1; PID:g32318  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C; F25-50/Domain: transmembrane #status predicted <TM1>  
F;62-93/Domain: transmembrane #status predicted <TM2>  
F;100-121/Domain: transmembrane #status predicted <TM3>  
F;142-168/Domain: transmembrane #status predicted <TM4>  
F;187-209/Domain: transmembrane #status predicted <TM5>  
F;367-387/Domain: transmembrane #status predicted <TM6>  
F;402-420/Domain: transmembrane #status predicted <TM7>  
F;2,12/Binding site: carbohydrate (Asn) #status predicted

Query Match 20.2%; Score 413; DB 2; Length 460;  
Best Local Similarity 27.4%; Pred. No. 9.7e-28;  
Matches 122; Conservative 84; Mismatches 150; Indels 90; Gaps 19;  
QY 5 NSTGILPPAAQVPLAFL---MSSFAFAIMVGNVAVILAFVVDRLNRHRSNFFFLNLAISD 61  
DB 12 NITVLAPGKGWQVAFIGITGLLSLATVGNLLVLSFKVNTLKTNNYFLLSLACAD 71  
QY 62 FLVGLISPLIPIPHVLF--NMNFGSGICMFWLITDYLCTASVYINVLISYDRYQSVNAV 120  
DB 72 LIIGTFSMNLYTYLLMGHWALGTACDLWALDYVAGSNVNMNLLISFDYFVSVTRPL 131  
QY 121 SYRAQHTGIMKIVQAV--WILAFVNGPMILASDSWKNSTNK-----DCEPGFVTEW 174  
DB 132 SYRAKRT--PRAALMIGLAVSFVWAPAIL---FWQYLVGERTVLGQCQYIQLSQP 186  
QY 175 YLITITMELLEPLVSVAYENVQIYWSLWKR-----RAL-----SRCPSHAGFTSSS 224  
DB 187 IITFGTAAAFYLPVTVMC---TLVWRIYRETNARELALQSGETPGKGGSSSSSE 242  
QY 225 AS-----GHLHRAGVACRT-----SNPGLKESAAASHSSSPRKK 258  
DB 243 RSQPGAEGSPETPPGCCR---CCRAPLLQAYSKEEEDGSGMESLTSSEGEFP--G 297  
QY 259 SSILVSL-----RTHMNSSITAFKVGSWFWSASA-----ALRQRY 294  
DB 298 SEWIKMPMVDPEAQAPKQPPRSSNTVKRGRERAGKQKPRGKEQLAKRTFSL 357  
QY 298 LRGRKLARSAILLSAFALCWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNP 357  
DB 358 VREKKAARTLSAILLAFITVTPYINMVLV-STFCCKDCVPETILW-ELGYWLCVYNSTNP 415  
QY 358 FLYPLCHRRFQKAFWKILCVTKW 380  
DB 416 MCYALCNKAFRDTF-RLLLLCRW 437

RESULT 3  
S09508  
muscarinic acetylcholine receptor M1 - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text\_change 21-Jul-2000  
C;Accession: S09508; S06327; S04326  
R;Chapman, C.G.; Brown, M.J.  
Nucleic Acids Res. 18, 2191, 1990  
A;Title: Isolation of the human m1 (Hml) muscarinic acetylcholine receptor gene by PCR  
A;Reference number: S09508; MUID:90245684; PMID:2336407  
A;Accession: S09508

Query Match 20.2%; Score 413; DB 2; Length 460;  
Best Local Similarity 27.4%; Pred. No. 9.7e-28;  
Matches 122; Conservative 84; Mismatches 150; Indels 90; Gaps 19;  
QY 5 NSTGILPPAAQVPLAFL---MSSFAFAIMVGNVAVILAFVVDRLNRHRSNFFFLNLAISD 61  
DB 12 NITVLAPGKGWQVAFIGITGLLSLATVGNLLVLSFKVNTLKTNNYFLLSLACAD 71  
QY 62 FLVGLISPLIPIPHVLF--NMNFGSGICMFWLITDYLCTASVYINVLISYDRYQSVNAV 120  
DB 72 LIIGTFSMNLYTYLLMGHWALGTACDLWALDYVAGSNVNMNLLISFDYFVSVTRPL 131  
QY 121 SYRAQHTGIMKIVQAV--WILAFVNGPMILASDSWKNSTNK-----DCEPGFVTEW 174  
DB 132 SYRAKRT--PRAALMIGLAVSFVWAPAIL---FWQYLVGERTVLGQCQYIQLSQP 186  
QY 175 YLITITMELLEPLVSVAYENVQIYWSLWKR-----RAL-----SRCPSHAGFTSSS 224  
DB 187 IITFGTAAAFYLPVTVMC---TLVWRIYRETNARELALQSGETPGKGGSSSSSE 242  
QY 225 AS-----GHLHRAGVACRT-----SNPGLKESAAASHSSSPRKK 258  
DB 243 RSQPGAEGSPETPPGCCR---CCRAPLLQAYSKEEEDGSGMESLTSSEGEFP--G 297  
QY 259 SSILVSL-----RTHMNSSITAFKVGSWFWSASA-----ALRQRY 294  
DB 298 SEWIKMPMVDPEAQAPKQPPRSSNTVKRGRERAGKQKPRGKEQLAKRTFSL 357  
QY 298 LRGRKLARSAILLSAFALCWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNP 357  
DB 358 VREKKAARTLSAILLAFITVTPYINMVLV-STFCCKDCVPETILW-ELGYWLCVYNSTNP 415  
QY 358 FLYPLCHRRFQKAFWKILCVTKW 380  
DB 416 MCYALCNKAFRDTF-RLLLLCRW 437

RESULT 4  
JT0531  
muscarinic acetylcholine receptor M5 - rat  
C;Species: Rattus norvegicus (Norway rat)

Query Match 20.2%; Score 413; DB 2; Length 460;  
Best Local Similarity 27.4%; Pred. No. 9.7e-28;  
Matches 122; Conservative 83; Mismatches 154; Indels 84; Gaps 18;  
QY 5 NSTGILPPAAQVPLAFL---MSSFAFAIMVGNVAVILAFVVDRLNRHRSNFFFLNLAISD 61  
DB 12 NITVLAPGKGWQVAFIGITGLLSLATVGNLLVLSFKVNTLKTNNYFLLSLACAD 71  
QY 62 FLVGLISPLIPIPHVLF--NMNFGSGICMFWLITDYLCTASVYINVLISYDRYQSVNAV 120  
DB 72 LIIGTFSMNLYTYLLMGHWALGTACDLWALDYVAGSNVNMNLLISFDYFVSVTRPL 131  
QY 121 SYRAQHTGIMKIVQAV--WILAFVNGPMILASDSWKNSTNK-----DCEPGFVTEW 174  
DB 132 SYRAKRT--PRAALMIGLAVSFVWAPAIL---FWQYLVGERTVLGQCQYIQLSQP 186  
QY 175 YLITITMELLEPLVSVAYENVQIYWSLWKR-----RAL-----SRCPSHAGFTSSS 224  
DB 187 IITFGTAAAFYLPVTVMC---TLVWRIYRETNARELALQSGETPGKGGSSSSSE 242  
QY 225 AS-----GHLHRAGVACRT-----SNPGLKESAAASHSSSPRKK 258  
DB 243 RSQPGAEGSPETPPGCCR---CCRAPLLQAYSKEEEDGSGMESLTSSEGEFP--G 297  
QY 259 SSILVSL-----RTHMNSSITAFKVGSWFWSASA-----ALRQRY 294  
DB 298 SEWIKMPMVDPEAQAPKQPPRSSNTVKRGRERAGKQKPRGKEQLAKRTFSL 357  
QY 298 LRGRKLARSAILLSAFALCWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNP 357  
DB 358 VREKKAARTLSAILLAFITVTPYINMVLV-STFCCKDCVPETILW-ELGYWLCVYNSTNP 415  
QY 358 FLYPLCHRRFQKAFWKILCVTKW 380  
DB 416 MCYALCNKAFRDTF-RLLLLCRW 437

RESULT 3  
S09508  
muscarinic acetylcholine receptor M1 - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text\_change 21-Jul-2000  
C;Accession: S09508; S06327; S04326  
R;Chapman, C.G.; Brown, M.J.  
Nucleic Acids Res. 18, 2191, 1990  
A;Title: Isolation of the human m1 (Hml) muscarinic acetylcholine receptor gene by PCR  
A;Reference number: S09508; MUID:90245684; PMID:2336407  
A;Accession: S09508

[illegible]

RESULT 6  
A29514  
muscarinic acetylcholine receptor M1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text\_change 24-Nov-1999  
C:Accession: A94518; A94293; A37121; A29514  
R:Bonner, T.I.  
submitted to GenBank, July 1987  
A:Reference number: A94518  
A:Accession: A94293  
A:Molecule type: mRNA  
A:Residues: 1-460 <B01>  
R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.  
Science 237, 527-532, 1987  
A:Title: Identification of a family of muscarinic acetylcholine receptor genes.  
A:Reference number: A94293; MUID:87263421; PMID:3037705  
A:Accession: A94293  
A:Molecule type: mRNA  
A:Residues: 1-227;338-460 <B02>  
A:Experimental source: cerebral cortex  
A:Note: only a part of the protein translation is given; none of the nucleotide sequence  
R:Kurténbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.  
J. Biol. Chem. 265, 13702-13708, 1990  
A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv  
A:Reference number: A37121; MUID:90337982; PMID:2380182  
A:Accession: A37121  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 62-124 <KUR>  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
F:25-50/Domain: transmembrane #status predicted <TM1>  
F:62-93/Domain: transmembrane #status predicted <TM2>  
F:100-121/Domain: transmembrane #status predicted <TM3>  
F:142-168/Domain: transmembrane #status predicted <TM4>  
F:187-209/Domain: transmembrane #status predicted <TM5>  
F:367-387/Domain: transmembrane #status predicted <TM6>  
F:402-420/Domain: transmembrane #status predicted <TM7>  
F:2.12/Binding site: carbohydrate (Asn) #status predicted

Query Match 20.0%; Score 410; DB 2; Length 460;  
Best Local Similarity 27.4%; Pred. No. 1.7e-27;  
Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;  
Qy 5 NSTGILPPAAQVPLAFL---MSSFAPAIMVGNNAVILAFVVDRLNRHSNYFFFLNLAISD 61  
Db 12 NITVLAPGKGPWQVAFIGITIGLLSLATVTGNLLVLSFKVNTLKTNNYFLLSLACAD 71  
Qy 62 FLVGLISIPLYIPHLVFNWFGSGICMFLITDYLLCTASVYNTVLISYDRYQSVNAV 120  
Db 72 LIIGTFSMNLTYTYLLMGHWALGTACDLMLADYVNASVWMLLLISFDYFVSVTRPL 131  
Qy 121 SYRAQHTGIMKIVQMVAW-WILAFVNGPMILASDSKNSNTNK-----DCEPGFVTEW 174  
Db 132 SYRAKET--PRAALMIGLAWLVSFLWAPAIL---FWQYLVGERTVLAGQCYIQFLSOP 186  
Qy 175 YILITMTLLEFLLPVISVAYFNVOIYWSLWKR-----RAL-----SRCPSHAGFTTSSS 224  
Db 187 IITFGTAMAAFYLPVTVMC-----TLYWRITYETENRARELAALQSGETPGKGGSSSSSE 242  
Qy 225 AS-----GHLHAGVACRT-----RTHNSSITAFKVGSWRSESA-----ALRQREY 294  
Db 243 RSQPGAEGSPSPGRCR---CCRAPRLLOAYSWKEEEDEGSMESLTSEGEPE--G 297  
Qy 259 SSILVSL-----RTHNSSITAFKVGSWRSESA-----ALRQREY 294  
Db 298 SEVVIKMPVDSEAAQPTKQPPKSPNTVKRPTKKG---RDRGGKGQKPRGKEQLAKRKT 354  
Qy 295 AELLRGRKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSF 354  
Db 355 FSLVKEKKAARTLSAILLAFILTWTPYINWLV-STFCKDCVPETLW-ELGWYLCVNST 412  
Qy 355 VNPFLYPLCHRRFQKAFWKILCVTKW 380  
Db 413 VNPFCYALCNKAFRDTF-RLLLLCRW 437

RESULT 8  
S47572  
muscarinic acetylcholine receptor m3 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text\_change 18-Feb-2000  
C:Accession: S47572  
R:Blee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.  
Biochim. Biophys. Acta 1223, 151-154, 1994  
A:Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 re  
A:Reference number: S47572; MUID:94339178; PMID:8061048  
A:Accession: S47572  
A:Status: preliminary  
A:Molecule type: mRNA

Db 413 VNPFCYALCNKAFRDTF-RLLLLCRW 437

RESULT 7  
I51837  
muscarinic receptor - rat  
C:Species: Rattus sp. (rat)  
C:Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text\_change 24-Nov-1999  
C:Accession: I51837  
R:Lai, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roeske,  
Adv. Exp. Med. Biol. 287, 313-330, 1991  
A:Title: The molecular properties of the M1 muscarinic receptor and its regulation of cy  
A:Reference number: I51837; MUID:92101806; PMID:1759615  
A:Accession: I51837  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-460 <RES>  
A:Cross-references: GB:S73971; NID:G241253; PIDN:AAB20705.1; PID:G241254  
C:Genetics:  
A:Gene: m1  
C:Superfamily: vertebrate rhodopsin

Query Match 20.0%; Score 410; DB 2; Length 460;  
Best Local Similarity 27.4%; Pred. No. 1.7e-27;  
Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;  
Qy 5 NSTGILPPAAQVPLAFL---MSSFAPAIMVGNNAVILAFVVDRLNRHSNYFFFLNLAISD 61  
Db 12 NITVLAPGKGPWQVAFIGITIGLLSLATVTGNLLVLSFKVNTLKTNNYFLLSLACAD 71  
Qy 62 FLVGLISIPLYIPHLVFNWFGSGICMFLITDYLLCTASVYNTVLISYDRYQSVNAV 120  
Db 72 LIIGTFSMNLTYTYLLMGHWALGTACDLMLADYVNASVWMLLLISFDYFVSVTRPL 131  
Qy 121 SYRAQHTGIMKIVQMVAW-WILAFVNGPMILASDSKNSNTNK-----DCEPGFVTEW 174  
Db 132 SYRAKET--PRAALMIGLAWLVSFLWAPAIL---FWQYLVGERTVLAGQCYIQFLSOP 186  
Qy 175 YILITMTLLEFLLPVISVAYFNVOIYWSLWKR-----RAL-----SRCPSHAGFTTSSS 224  
Db 187 IITFGTAMAAFYLPVTVMC-----TLYWRITYETENRARELAALQSGETPGKGGSSSSSE 242  
Qy 225 AS-----GHLHAGVACRT-----RTHNSSITAFKVGSWRSESA-----ALRQREY 294  
Db 243 RSQPGAEGSPSPGRCR---CCRAPRLLOAYSWKEEEDEGSMESLTSEGEPE--G 297  
Qy 259 SSILVSL-----RTHNSSITAFKVGSWRSESA-----ALRQREY 294  
Db 298 SEVVIKMPVDSEAAQPTKQPPKSPNTVKRPTKKG---RDRGGKGQKPRGKEQLAKRKT 354  
Qy 295 AELLRGRKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSF 354  
Db 355 FSLVKEKKAARTLSAILLAFILTWTPYINWLV-STFCKDCVPETLW-ELGWYLCVNST 412  
Qy 355 VNPFLYPLCHRRFQKAFWKILCVTKW 380  
Db 413 VNPFCYALCNKAFRDTF-RLLLLCRW 437

RESULT 8  
S47572  
muscarinic acetylcholine receptor m3 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text\_change 18-Feb-2000  
C:Accession: S47572  
R:Blee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.  
Biochim. Biophys. Acta 1223, 151-154, 1994  
A:Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 re  
A:Reference number: S47572; MUID:94339178; PMID:8061048  
A:Accession: S47572  
A:Status: preliminary  
A:Molecule type: mRNA

A;Residues: 1-590 <LEE>  
A;Cross-references: EMBL:U08286; NID:g520465; PIDN:AAA51866.1; PID:g520466  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: neurotransmitter receptor

Query Match 20.0%; Score 409.5; DB 2; Length 590;  
Best Local Similarity 25.0%; Pred. No. 2.6e-27;  
Matches 126; Conservative 83; Mismatches 134; Indels 161; Gaps 17;

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Qy      18  LAFIMSSFAFALMGVAVILAFVVDNRNLHRSNFYFFNLALISDFVGLTIPDIYIPHL  77
      :||| - :|||:||| : : :|||:||| :|||:||| :||| : : :
Db      71  IAFPTGVLALWTIIIGNLIVIVAFKNQKLTVMNYFLLSLACADLIIGVISNNFTFYII  130

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Qy 78 FN-WNFGSGICMEWLIITDYLLCTASVNVILISYDRYQSVNASVYRAQHT---GIMKI 132

Db 131 MNRWALGNLACDLWLSIDYVNASVNMVLLISFDRYFSTIRPTRYAKRTTKRAGVWIG 190

```

Qy 133 VAQWVAWVIAFLVNGPMILASDWKNSWTKDCEPG-----FVTEWYILITIMLSELL 187
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 191 LA-----WVISFILWAPAIL--FWQYFVGKRTVPGCCETQIFUSEETIFGTAAAFYM 242
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

**Oy** 188 PVISVAVNFQIYWSLWKRRALSRCPSHAGF--STTSSASGHLHAGVACRTSNPLKE 245  
| | : | : | | | | : | : | : | : | : | :  
**Dd** 243 PVTIMTI---LYMRIYKTE-KTKELAGIQASGTAEAEFNVPHTGSGRSSCSSEYLQQ 297

Qy	246	SAASR	-----	HSES	-----	254
		:				
Db	298	QSMRGARRKYGRCHF	WFTTKSNKPSAEQMDQDHSSSDSNWNDAASLENSASSDEEDI			357

QY 255 ---PRKKSSILVSLRTH---MNS---SITAPKV----- 278  
 Db 358 GSETRAIYSLVLKPGHSTILNKLPSDDLQVPEELGSGVLERKPSKLTQTCQSMDDG 417

Qy	279	GFWR-	-----ESAA-	-----	LRQ	291
		:				
Db	418	GSQSFSLPIQESAVDTAKADYNSSVGKTTATLPLSFKEATLAKRPALKTRQITK			:	477

QY 292 REVAELLGRKLSARLAILLSAPACWAPCYCLFTIIVLTSTVPRTERPKSVWYSTAFMLQWF 351  
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :  
Db 478 RKRMSLIKEKGAQTLSAILLAPIITWTPTPNIMVLV-NTFCDSICPRTYW-NUGYWCYII 535

QY 352 NSEVNPFLYPLCHRRFQKAFWKIL 375  
|| ||| ||:| :| :|  
Db 536 NSTVNPVCYALCNKTRFTFKML 559

RESULT 9  
A29476  
muscarnic acetylcholine receptor MA

C.Species: Rattus norvegicus (Norway rat)  
C.Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Feb-2000  
C.Accession: A29476  
R.Braun, T. Schofield, B. B. Shivare, B. B. Shivare, B. B. Shivare

Biochem. Biophys. Res. Commun. 149, 125-132, 1987

A;Molecule type: mRNA  
A;Residues: 1-589 <BRA>  
A;Cross-references: GB:M18088; NID:g202657; PIDN:AAA40659.1; PID:g202658  
A;Experimental source: brain

C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor;  
F:167-90/Domain: transmembrane #status predicted <TM>  
F:104-124/Domain: transmembrane #status predicted <TM>

Domain	transmembrane	#status	predicted
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F.184-206/Domain	transmembrane	#status	predicted
F.230-251/Domain	transmembrane	#status	predicted
F.492-512/Domain	transmembrane	#status	predicted

Domain: transmembrane #status predicted <TM>  
 F:527-545/Domain: transmembrane #status predicted <TM>  
 Query Match 19.7% Score 403; DB 2; Length 589;  
 Best Local Similarity 23.9% Posed vs. 0.2-2.27

--- more community 23.0%; FIED. NO. 9.2E-7;;

Matches	125;	Conservative	84;	Mismatches	145;	Indels	172;	Gaps	15;
QY	4	SNSTGILPPAAQ-----YPLAFLMSSFAFAITWGNNAVILAFVVDRLNLRHRSNYFFNL	58						
Db	51	SNDTSSDPLGGHTITQWVFIAFLTGFLALVTIIIGNILVIVAFKYNKQLKTNNYFLLSLA	110						
QY	59	ISDFVLVLGISLPIYPIHVLFN-WNFGSGICMFWLITDYLLCTASVYNNIVLISVDYQSVS	117						
Db	111	CADLIIGVISMNLFTTYIIMNRWALGNLACDLWLSIDVYASNASVMNLVISFDYPSIT	170						
QY	118	NAVSRAQHT-----GIMKIVAQMVAVILAPLVNGPMILASDSMKNSTNTKDCBPG---	169						
Db	171	RPLTYRAKRTTKRAGVMIGLA-----WVISFLWAPAIL---FWQYFVGKRTVPGECFI	222						
QY	170	-FVTEWYILITITMLLEFLLPVISVAYENVQIYWSLWKRRALSCPSHAGF--STTSSAS	226						
Db	223	QFLSEPIITFTGATAAFYMPVTIMTI---LYMRIYKETE-KRTKELIAGLQASGTAEABE	277						
QY	227	GHLHRAGVACTSNPGIKESAAHSRHSPPRK-----SSILVSLRTHMNSSI-----	273						
Db	278	NFVHPTGSSRSCSYELQQGVKRA---SSRRKYGRCHFMTTKSWKPSAQMDQDHSSTD	334						
QY	259	-----SSILVSLRTHMNSSI-----	273						
Db	335	SWNNDDAAASLENSASSDEBDIGSETRAIYSIVLKFLPGHSSIINSTKLPSSDNLQVSNED	394						
QY	274	-----TAPKVGSGFWRESAA-----	288						
Db	395	LGTVDVERNAHKLOAKSGMGDGNCKQDFTKLPILQLESVDTGKTSDDTSSADKTTATLP	454						
QY	289	-----LRQREYAEILGRKLARSAILLISAFACIWAICYCLFIVLS	329						
Db	455	LSFKEATLAKRFALKTRSQITTKRMSLIKEKAAQTLTSAILLAFIITWPTNIMVLV-N	513						
QY	330	TYPTERTPKSVYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKIL	375						
Db	514	TFRDSCLPKTYW-NUGWLCYINSTNPVCYALCNKTFITTFKMLL	558						

RESULT 10

S10128 muscarinic acetylcholine receptor M4 - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 18-Feb-2000  
C:Accession: S10128  
P:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A>Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of human M4 muscarinic acetylcholine receptors  
A:Reference number: S04326; MUID:80166632; PMID:3443095

A;Accession: S10128  
A;Molecule type: DNA  
A;Residues: 1-590 <PER>  
A;Cross-references: EMBL:X15266; NID:g32323; PID:CAA33337.1; PID:g32324  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane  
F;68-95/Domain: transmembrane #status predicted <TM1>  
F;105-131/Domain: transmembrane #status predicted <TM2>  
F;143-164/Domain: transmembrane #status predicted <TM3>  
F;185-207/Domain: transmembrane #status predicted <TM4>  
F;231-252/Domain: transmembrane #status predicted <TM5>  
F;493-513/Domain: transmembrane #status predicted <TM6>  
F;525-546/Domain: transmembrane #status predicted <TM7>  
F;5,6,15,41/Binding site: carboxhydrate (Asn) (covalent) #status predicted

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Query Match      19.7%;   Score 402.5;   DB 2;   Length 590;
Best Local Similarity 24.0%;   Pred. No. 1e-26;
Matches 121;   Conservative 86;   Mismatches 135;   Indels 163;   Gaps 16;

QY      18  LAFELMSFAFAIMGVNAWVILAFVVDVDRHRHSYFFNLALISDFLVLGLSIFLYIPHVL 77
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Db      71  IAFLTGLAVTTIIGNLIVIVSFKNVQLKTVNNYFLLSLACADLIIGVISMNLEFTTVII 130

QY      78  FN-WNFGSGICMFWLITDYLCLLTASVYNIVLISYDRYQSVSNVSVYRAQHT- ---GIMKI 132

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Db 131 MNRWALGNLACDLWLAIDYASNASVWMLLVISDFRYSITRLTYRAKRTTKRAGWIG 190  
 QY 133 VAQWVAVWILAFVNGPMILASDWSKNTKDCBPG-----FVTEWYILITIMLLEFLL 187  
 Db 191 LA-----WVLSFVWAPAIL---FWQYFVGKRTVPGECEFIQELSEPTITFGTAIAAFYM 242  
 QY 188 FVLSVAVFNVQIYWSLWK----- 205  
 Db 243 PVTIMTI---LWRIYKETEKRTELKELAGLQASGTEAETENFVHPTGSSSCSSYELQQQ 298  
 QY 206 -----RRALSRCBHGAGPTT-----SSASCHLRHAGVACKTSNPGLES 246  
 Db 299 SMKRSNRKYGRC--HFWFTKSWKPSSEQMDQDQSSSDSWNNDDAAASLENSASDEED 356  
 QY 247 AASR-----HS----- 252  
 Db 357 IGSETRAIYIVLKLPGHSTILNKLPSDDNLQVPEELGMVDLKERKADKLQAKSVDD 416  
 QY 253 --ESPRLKSSILVSLR-----THNNSI-----TAFKVGSS-----FWRSESAALR 290  
 Db 417 GGSPPKGSFKLPIQLESADVDTAKTSDVNSVSGKSTATLPLSFKEATLAKRFALKTRSQIT 476  
 QY 291 QREYAEILLRGRKLARSAILLSAFACWAPVCLFTIVLSTYPRTERPKSVWYSIAFWLQW 350  
 Db 477 KRKMSLVKEKAAQTLASAILLAFITITPTYNIMVLV-NTFCDSCIPKTFW-NLGYWLCY 534  
 QY 351 FNSFVNPFYPLCHRRFOKAFWKIL 375  
 Db 535 INSTVNPVCYALCNKTFRTFMULL 559  
 RESULT 11  
 B29514  
 muscarinic acetylcholine receptor M3 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 18-Feb-2000  
 C:Accession: B94518; B94293; B37121; B29514  
 R:Bonner, T.I.  
 submitted to GenBank, July 1987  
 A:Reference number: A94518  
 A:Accession: B94518  
 A:Molecule type: mRNA  
 A:Residues: 1-589 <BO1>  
 R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.  
 Science 237, 527-532, 1987  
 A:Title: Identification of a family of muscarinic acetylcholine receptor genes.  
 A:Reference number: A94293; MUID:87263421; PMID:3037705  
 A:Accession: B94293  
 A:Molecule type: mRNA  
 A:Residues: 1-269;463-589 <BO2>  
 A:Experimental source: cerebral cortex  
 A:Note: only a part of the protein translation is given; none of the nucleotide sequence  
 R:Kurtenschach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.  
 J. Biol. Chem. 265, 13702-13708, 1990  
 A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv  
 A:Reference number: A37121; MUID:90337982; PMID:2380182  
 A:Accession: B37121  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 104-166 <KUR>  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme  
 F:67-90/Domain: transmembrane #status predicted <TM1>  
 F:104-124/Domain: transmembrane #status predicted <TM2>  
 F:142-163/Domain: transmembrane #status predicted <TM3>  
 F:184-206/Domain: transmembrane #status predicted <TM4>  
 F:230-251/Domain: transmembrane #status predicted <TM5>  
 F:492-512/Domain: transmembrane #status predicted <TM6>  
 F:527-545/Domain: transmembrane #status predicted <TM7>  
 F:6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 19.6%; Score 402; DB 2; Length 589;

Best Local Similarity 23.8%; Pred. No. 1.1e-26;  
 Matches 125; Conservative 84; Mismatches 145; Indels 172; Gaps 15;  
 QY 4 SNSTGLPRAAQ-----VPLAFLMSSFAFPAIMVGNVAVILAFVVDRLNLRHSNYFFLNLA 58  
 Db 51 SNTSDSPLGGHTIMQVVFIAFLTGFLALVTIIGNILVIVAFKVNKQKLTNNVFLSLA 110  
 QY 59 ISDFLVGLISIPLYIPIHVLFN-WNFGSGICMFWLITDYLLCTASVNVILISVDYQSUS 117  
 Db 111 CADLLIGVISMNLFTTIIIMRWALGNLACDLWLSIDYASNASVWMLLVISDFRYSIT 170  
 QY 118 NAVSYRAOHT-----GIMKIVAVWVILAFVNGPMILASDWSKNTKDCBPG--- 169  
 Db 171 RPLTYRAKRTTKRGGVMIGLA-----WVLSFVWAPAIL---FWQYFVGKRTVPGECEFI 222  
 QY 170 -FVTEWYILITIMLLEFLLPVISVAVENVOIYWSLMKRRALSRCPSHAGF--STTSSAS 226  
 Db 223 QELSEPTITGTALAAFYMPVTIMTI---LYWRIYKETE-KRTKELAGLQASGTEAEAE 277  
 QY 227 CHLRAGVACRTSNPGLESAAASHSESPPRK----- 258  
 Db 278 NFVHPTGSSSCSSYELQQGVKR---SSRRKYGRCHFHTTKSWKPSAEQMDQDQSSSD 334  
 QY 259 -----SSILVSLRTHMNSSI----- 273  
 Db 335 SWNNDDAAASLENSASDEEDIGSETRAIYIVLKLPGHSSILNKLPSDDNLQVSNED 394  
 QY 274 -----TAFKVGFSFWRSESA----- 288  
 Db 395 LGTVDVERNAHKLQAKSMGDCNQDFTKLPLOLESADVDTGKTSIDNSSADKTTATLP 454  
 QY 289 -----LFQREYAEILLRGRKLARSAILLSAFACWAPVCLFTIVLS 329  
 Db 455 LSFKEATLAKRFALKTRSQITKRRKMSLIKEKAAQTLASAILLAFITITPTYNIMVLV-N 513  
 QY 330 TYPRTERPKSVWYSIAFWLQWNSFVNPFYPLCHRRFOKAFWKIL 375  
 Db 514 TFCDSICPIKTFW-NLGYWLCYINSTVNPVCYALCNKTFRTFMULL 558  
 RESULT 12  
 A55019  
 muscarinic acetylcholine receptor, M3 isoform - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 21-Jul-2000  
 C:Accession: A55019  
 R:Gadbut, A.P.; Galper, J.B.  
 J. Biol. Chem. 269, 25823-25829, 1994  
 A:Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and  
 A:Reference number: A55019; MUID:95014393; PMID:7929287  
 A:Accession: A55019  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-639 <GAD>  
 A:Cross-references: GB:L10617; NID:9530097; PIDN:AAA65961.1; PID:9530098  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: neurotransmitter receptor  
 Query Match 19.6%; Score 401; DB 2; Length 639;  
 Best Local Similarity 24.4%; Pred. No. 1.5e-26;  
 Matches 124; Conservative 84; Mismatches 136; Indels 164; Gaps 16;  
 QY 16 VPLAFLMSSFAFPAIMVGNVAVILAFVVDRLNLRHSNYFFLNLAISDFLVGLISIPLYIHP 75  
 Db 117 VLIAFITGIALVTIIGNILVIVSFKNQKLTNNVFLSLACADLIIGVISMNLFTTY 176  
 QY 76 VLP-WNFGSGICMFWLITDYLLCTASVNVILISVDYQSUSVAVYRAOHT-----GIM 130  
 Db 177 IIMGHWALGNLACDLWLSIDYASNASVWMLLVISDFRYSITRPLTYRAKRTTKRAGVM 236  
 QY 131 KIVAQWVAVWVILAFVNGPMILASDWS-----KNSTNTKDCBPGFVTEWYILITIMLEF 185  
 Db 237 IGIA-----WVLSFVWAPAIL---FWQYFVGKRTVPDLDECFTQFLSEPIITFTGTAIAAF 288

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QY 186 LLPVISAAYFNQVYIWSLWKRALLRCPCHAGFTSTSSA--SGHLHRAGVACRTSNGL 243
Db 289 YLPVTIMSI-----LYWRIYKETE-KRTKELAGLQASGEATAPVHQTGSRSLSYEL 343
QY 244 KESASRHSSESPRKS----- 259
Db 344 QRQSTKSSRRKRYRCHFWLTMKWEPTDQGOEHSSSDSWNNNDAAASLSSASSDEE 403
QY 260 -----SILSLRTH-----MNSSITAFKV----- 278
Db 404 DITAEITAIYSIVLKLPHSAILNSTKLPPSSDELNEGADLOKSDTSQEKPKKLOPPK 463
QY 279 -----GSFWS-----BSAAL----- 289
Db 464 SIQDGSFQKFSKLPQPGSAETATASDGISSVTKTSAAALPLSFKEATLAKKFAKTR 523
QY 290 --RQREYAEILLRGRKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFW 347
Db 524 QITRKMSLIKKEKAACTISAILFAIITWTPTYNIMLV-NTFCDGV-PKTVN-NLGYW 580
QY 348 LOWFNSFVNPLFLPCHRRRQKAFWKIL 375
Db 581 LCVINSTVNVFCALCKMFRNIFKMLL 608

```

## RESULT 13

A31897  
 muscarinic acetylcholine receptor M1 - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 24-Nov-1999  
 C:Accession: A31897  
 R:Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.  
 J. Biol. Chem. 263, 18397-18403, 1988  
 A>Title: Isolation, sequence, and functional expression of the mouse M1 muscarinic acetylcholine receptor.  
 A:Reference number: A92694; MUID:89054021; PMID:2848036  
 A:Accession: A31897  
 A:Molecule type: DNA  
 A:Residues: 1-460 <SHA>  
 A>Note: the authors translated the codon ATC for residue 119 as Thr  
 R:Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.  
 J. Biol. Chem. 264, 6596, 1989  
 A:Reference number: A92742  
 A:Contents: annotation; erratum, correct translation of residue 119  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C; G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C

F:25-50/Domain: transmembrane #status predicted <TM1>  
 F:62-93/Domain: transmembrane #status predicted <TM2>  
 F:100-121/Domain: transmembrane #status predicted <TM3>  
 F:142-168/Domain: transmembrane #status predicted <TM4>  
 F:187-209/Domain: transmembrane #status predicted <TM5>  
 F:367-387/Domain: transmembrane #status predicted <TM6>  
 F:402-420/Domain: transmembrane #status predicted <TM7>

Query Match 19.5%; Score 400; DB 2; Length 460;  
 Best Local Similarity 27.0%; Pred. No. 1.3e-26;  
 Matches 120; Conservative 86; Mismatches 152; Indels 86; Gaps 19;

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QY 5 NSTGILPAAQVPLAFLMSS---FAFAMVGNVAVILAFVVDNLRHRSNYFFLNLAISD 61
Db 12 NITVLAPCKGPQWAFIGSTGLLSLAVTGTGLLALDYVNASVWNLISIKVNTLKVNNYFLLSLACAD 71
QY 62 FLVGLISILPIYIPHYLF-NNWFGSGICMFLLITDYLCTASVYNNVILSYDRYQSVSNV 120
Db 72 LIIGTFSMNLYTYLLMGHWALGTLCADLWALDYVNASVWNLISIKVNTLKVNNYFLLSLACAD 131
QY 121 SYRAQHTGIMKIVAOMVAV-WILAFVNGPMILASDSWKNSTNTK-----DCEPGFVTEW 174
Db 132 SYRAKRT--PRAALMIGLAMVSVFLWAPAIL--FWQLVGVRTVLGQCYYQLFSLQP 186
QY 175 YILITLMLLEFLPLVISYAYFNQVYIWSLWKR-----RAL-----SRCPSHAGFTSTSSS 224
Db 187 IITGTMAAFYLPVTVMC-----TLYWRIYRETNARELAALQSGSETPGKGGGSSSSSE 242

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QY 225 AS-----GHLHRAGVACRT-----SNPGLKESAAHRHSSEPRRK 258
Db 243 RSQFCAEGSPSPPCRCR---CCRAPLLQAYSWKBEEDDEGSWESLTSSEGEP--G 297
QY 259 SSILVSL-----RTHMNSSITAFK-----VGSFWRSESALRQREYAE 296
Db 298 SEVVIKPMVDPEAQAPTKQPKSPNTVRPTTKGRDRGGKQKPRGKEQMAKRKTES- 356
QY 297 LLRGRKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVN 356
Db 357 LVKEKKAARTLSAILLAFILWTPTYNIMLV-STFCKDCVPETLW-ELGYWLCYVNSTVN 414
QY 357 PFLYPLCHRRRQKAFWKILCVTKW 380
Db 415 FMCYASCNKAFRDHF-RLLLICRW 437

```

## RESULT 14

JT0530

muscarinic acetylcholine receptor M5 - human

C:Species: Homo sapiens (man)

C&gt;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 21-Jan-2000

C:Accession: JT0530

R:Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.

Neuron 1, 403-410, 1988

A&gt;Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor.

A:Reference number: JT0530; MUID:90166521; PMID:3272174

A:Accession: JT0530

A:Molecule type: DNA

A:Residues: 1-532 &lt;BON&gt;

C:Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neurotransmitter acetylcholine.

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C; G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C

F:30-53/Domain: transmembrane #status predicted &lt;TM1&gt;

F:67-87/Domain: transmembrane #status predicted &lt;TM2&gt;

F:105-126/Domain: transmembrane #status predicted &lt;TM3&gt;

F:147-169/Domain: transmembrane #status predicted &lt;TM4&gt;

F:192-214/Domain: transmembrane #status predicted &lt;TM5&gt;

F:444-464/Domain: transmembrane #status predicted &lt;TM6&gt;

F:479-498/Domain: transmembrane #status predicted &lt;TM7&gt;

F:8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.5%; Score 399.5; DB 2; Length 532;  
 Best Local Similarity 24.6%; Pred. No. 1.6e-26;  
 Matches 122; Conservative 90; Mismatches 142; Indels 141; Gaps 15;

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QY 16 VPLAFIMSSFAIMVGNVAVILAFVVDNLRHRSNYFFLNLAISDPLVGLISILPIYIPH 75
Db 31 ITIAAVTVVSLIITVGNVLMISFKVNSQLKTVNNYLLSLACADLISGIFSMNLYTT 90
QY 76 VLF-NNWFGSGICMFLLITDYLCTASVYNNVILSYDRYQSVSNVAVSYRAQHT---GTM 130
Db 91 ILMGHWALGTLCADLWALDYVNASVWNLISIKVNTLKVNNYFLLSLACADLISGIFSMNLYTT 150
QY 131 KIVAOMVAVILAFVNGPMILASDSW-----KNSTNTKDCPEPGFVTEWYILITMLLEF 185
Db 151 IGLA-----WLISFILWAPAILC---WQYLVGKRTVPLDECOQLSEPTITFGTAAAP 202
QY 186 LLPVISYAYFNQVYIWSLWKR-----RALSRCP----- 213
Db 203 YIPVSMVTLICRYIRETEKTKDLADLQSDSVTKAEKRPAPRALFRSLCRLCPRTLA 262
QY 214 ----SHAGFTST--SSSASGHLHRAG-----VACRT-----SNPGLK 244
Db 263 QRERNQASWSSSRSTSTTGKPSQATGPSANWAKAEQUTTCSSYFSSDEDEKDPATDVLQ 322
QY 245 ESAASRHSSESPRKSILVSLRTHMNSSI--TAFKVGSGFWRSESAAALR----- 290
Db 323 VVYKSGKESGPEGFSABETEETEVKAETEKSDYDTNLYLLSPAAHRPKSQKCVAYKFR 382
QY 291 -----OREYAEILLRGRKLAR 305

```

Mon Oct 4 10:27:28 2004

Db 383 LVVADGNQETNNGCHVKIMPCPEFPVAKPESTKGLNPNBHQMTKRKRVLVVKERKAAQ 442  
 QY 306 SLAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWVSIWQWNSFVNPLYPLCHR 365  
 Db 443 TLSAILLAFITITPTNIMLV-STFCDKCVPTLWH-LGYWLCYVNSTVNPICAYLCNR 500  
 QY 366 RFOKAFWKILCVTKW 380  
 Db 501 TFRKTF-KMULLCRW 514

RESULT 15  
 S71323  
 alpha-1A adrenergic receptor - Japanese medaka  
 C;Species: Oryzias latipes (Japanese medaka)  
 C;Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 17-Mar-1999  
 C;Accession: S71323  
 R;Yasuoka, A.; Abe, K.; Arai, S.; Emori, Y.  
 Eur. J. Biochem. 235, 501-507, 1996  
 A;Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Me  
 A;Reference number: S71323; MUID:96184522; PMID:8654394  
 A;Accession: S71323  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-477 <YAS>  
 A;Cross-references: EMBL:D63859  
 A;Note: it is uncertain whether Met-1 or Met-8 is the initiator  
 C;Superfamily: vertebrate rhodopsin

Query Match 19.2%; Score 392.5; DB 2; Length 477;  
 Best Local Similarity 28.0%; Pred. No. 5.8e-26;  
 Matches 115; Conservative 65; Mismatches 145; Indels 85; Gaps 15;

QY 4 SNSTGILPP-----AAQVPLAFIMSSFAFAMVGNVAVILAFVVDNLRHRSNYFELNLAI 59  
 Db 18 SNCSHVLAPELNTKAVLVGMVLGIFLFGVIGNILVLSVCHRLQTVTVYFIVNLAV 77  
 QY 60 SDFVLGLISIP-L-YIPHLFNNFGSGICMEWLIITDYLLCTASVNVNVLISYDRYQSVSN 118  
 Db 78 ADLLSSTVLPFSAIFELDRWVGRVFCNIWAAVDVLCCTASIMSLCVISYDRYIGVSY 137  
 QY 119 AVSYRAQHTGIMKIVAQMVAVWILAFVNV-GPMILASDSWKNSTNTKD--C-----EPGFV 171  
 Db 138 PLRYPAIMTKRALLAVML-LWLVSVIISIGLFL---GWKEPAPEDETVCKITEEPGYA 192  
 QY 172 TEWYILTITMLLEFLLPVISVAYFNVQIYVSLWKRRLSRCPSHAGFTTSSSASGHLHR 231  
 Db 193 -----IPSAVGSFYPLAAILAWYCRVY----- 215  
 QY 232 AGVACRTSNPGIKESASRHSSEPREKSSILYSLRTHMNSSITAPKVGSEFWSESAALRQ 291  
 Db 216 --VVAQKESRGLKEGQKIEKSDSEQ-----VILRMHGRNTTV-----SEDEALRS 258  
 QY 292 REVAEL-----LRGRKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWVSIAP 346  
 Db 259 RTHFALRLLKFSREKKAATLGIVGCVLWLPFELVLPISGIFP-AYRPSDTVFKITF 317  
 QY 347 WLQWFNSFVNPLYPLCHRRFQKAFWKIL---CVTKWPA-----LSQNQS 388  
 Db 318 WLGYFNCSNPIITILCSNQEFKAKFOSLLGVHCLRMTPRAHHHLSVGOS 367

Search completed: October 1, 2004, 10:13:03  
 Job time : 21 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:05:12 ; Search time 13 Seconds  
(without alignments)  
1566.110 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPAISQNSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1370.5	66.9	390	1	HH4R_HUMAN
2	722.5	35.3	445	1	HH3R_HUMAN
3	721.1	35.0	445	1	HH3R_CAVPO
4	716.5	35.0	445	1	HH3R_RAT
5	715.5	34.9	445	1	HH3R_MOUSE
6	418.0	20.4	460	1	ACM1_WACMU
7	414.5	20.2	532	1	ACM5_WACMU
8	413.0	20.2	460	1	ACM1_HUMAN
9	413.0	20.2	460	1	ACM1_PIG
10	410.5	20.0	531	1	ACM5_RAT
11	410.5	20.0	590	1	ACM3_PIG
12	410.0	20.0	460	1	ACM1_RAT
13	409.5	20.0	590	1	ACM3_BOVIN
14	408.0	19.9	585	1	ACM3_CAEEL
15	404.5	19.8	532	1	ACM5_HUMAN
16	404.0	19.7	589	1	ACM3_MOUSE
17	403.5	19.7	590	1	ACM3_PONPY
18	402.5	19.7	590	1	ACM3_GORGO
19	402.5	19.7	590	1	ACM3_HUMAN
20	402.5	19.7	590	1	ACM3_PANTR
21	402.0	19.6	589	1	ACM3_RAT
22	401.0	19.6	460	1	ACM1_MOUSE
23	401.0	19.6	639	1	ACM3_CHICK
24	394.5	19.3	576	1	AIAD_RABIT
25	393.0	19.2	444	1	OAR_CAEEL
26	393.0	19.2	562	1	AIAD_MOUSE
27	392.5	19.2	470	1	AIAD_ORYLA
28	392.0	19.1	490	1	AIAD_CHICK
29	390.5	19.1	400	1	D3DR_CERAE
30	389.5	19.0	400	1	D3DR_HUMAN
31	389.5	19.0	515	1	AIAB_MESAU
32	388.5	19.0	515	1	AIAB_RAT
33	388.5	19.0	491	1	HH1R_BOVIN

#### ALIGNMENTS

##### RESULT 1

ID	HH4R_HUMAN	STANDARD;	PRT;	390 AA.
AC	Q9H3N8; Q9GZQ0;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105)			
DE	(GPCR105) (SP9144) (AXOR35).			
GN	HRH4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]_TaxID:9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20538417; PubMed=10973974;			
RA	Oda T., Morikawa N., Saito Y., Matsumoto S.-I.;			
RT	"Molecular cloning and characterization of novel type of histamine			
RT	receptor preferentially expressed in leukocytes.";			
RL	J. Biol. Chem. 275:36781-36786(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	TISSUE=Leukocyte;			
RX	MEDLINE=20568725; PubMed=11118334;			
RA	Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;			
RT	"Molecular cloning and characterization of a new human histamine			
RT	receptor, HH4R.";			
RL	Biochem. Biophys. Res. Commun. 279:615-620(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Jones P.G., Wu S., Betty M.;			
RT	"Cloning of a novel histamine receptor.";			
RT	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	TISSUE=Bone marrow;			
RX	PubMed=11179434;			
RA	Liu C., Ma X.-J., Jiang X., Wilson S.-J., Hofstra C.L., Blevitt J.,			
RA	Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.;			
RT	"Cloning and pharmacological characterization of a fourth histamine			
RT	receptor (H4) expressed in bone marrow.";			
RL	Mol. Pharmacol. 59:420-426(2001).			
RN	[5]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	TISSUE=Eosinophil;			
RX	MEDLINE=21104636; PubMed=11181941;			
RA	Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A.,			
RA	Antes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,			
RA	Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,			
RA	Monma F.J. Jr.;			
RT	"Cloning and characterization of a novel human histamine receptor.";			
RL	J. Pharmacol. Exp. Ther. 296:1058-1066(2001).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21106320; PubMed=11179436;			

P25100 homo sapien  
P70174 mus musculu  
P35367 homo sapien  
Q9n2b2 pan troglod  
P31389 cavia porce  
P97717 mus musculu  
P35368 homo sapien  
P23944 rattus norv  
P08173 homo sapien  
P08172 homo sapien  
Q91081 labrus ossi  
P10980 rattus norv

RA Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J.,  
RA Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L.,  
RA Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,  
RA Bergma D.J., Fitzgerald L.R.;  
RT "Cloning, expression, and pharmacological characterization of a novel  
RT human histamine receptor";  
RL Mol. Pharmacol. 59:434-441(2001).  
[7]  
RN SEQUENCE FROM N.A.  
RP O'Reilly M.A.;  
RA "Identification of a histamine H4 receptor on human eosinophils - Role  
RT in eosinophil chemotaxis";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
[8]  
RN SEQUENCE FROM N.A.  
RP Puhl H.L. III, Ikeda S.R., Aronstam R.S.;  
RT "cDNA clones of human proteins involved in signal transduction  
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: The H4 subclass of histamine receptors could mediate the  
CC histamine signals in peripheral tissues. Displays a significant  
CC level of constitutive activity (spontaneous activity in the  
CC absence of agonist).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and  
CC eosinophils. Shows preferential distribution in cells of  
CC immunological relevance such as T-cells, dendritic cells,  
CC monocytes, mast cells, neutrophils. Also expressed in a wide  
CC variety of peripheral tissues, including the heart, kidney, liver,  
CC lung, pancreas, skeletal muscle, prostate, small intestine,  
CC spleen, fetal liver and lymph node.  
CC -!- INDUCTION: Expression is either up-regulated or down-regulated  
CC upon activation of the lymphoid tissues and this regulation may  
CC depend on the presence of IL-10 or IL-13.  
CC -!- MISCELLANEOUS: Does not bind diphenhydramine, lorazepam,  
CC ranitidine, cimetidine and chlorpheniramine. Shows modest affinity  
CC for dimaprit, imipramine and imetit. The order of inhibitory activity  
CC was imetit > clobenpropit > burinamide > thioperamide.  
CC Clobenpropit behaves as a partial agonist, dimaprit and  
CC imipramine show some agonist activity while clozapine behaves as  
CC a full agonist. Thioperamide shows inverse agonism (enhances cAMP  
CC activity). The order of inhibitory activity of histamine  
CC derivatives was Histamine > N-alpha-methylhistamine > R(-)-alpha-  
CC methylhistamine > S(+)-alpha-methylhistamine. Both N-alpha-  
CC methylhistamine > R(-)-alpha-methylhistamine behave as full  
CC agonists.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AB044934; BAB13698.1; -  
CC EMBL; AB045370; BAB20091.1; -  
CC EMBL; AF307973; AAG32052.1; -  
CC EMBL; AF312230; AAK12081.1; -  
CC EMBL; AF323449; AAK43542.1; -  
CC EMBL; AF325356; AAL01684.1; -  
CC EMBL; AJ298292; CAC83493.1; -  
CC EMBL; AY136745; AAN01271.1; -  
CC PIR; JC7566; JC7566.  
CC Genew; HGNC:17383; HRR4.  
CC MIM; 606792; -; C:integral to membrane; NAS.  
CC GO; GO:0016021; C:integral to membrane; NAS.  
CC GO; GO:0004969; F:histamine receptor activity; NAS.  
CC InterPro; IPR000276; GPCR\_Rhodopsin.  
CC InterPro; IPR008102; Histamine\_H4.  
CC Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR00237; GPCR RHODOPSIN.  
DR PRINTS; PR01726; HISTAMINEH4R.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.  
DR PROSITE; PS02622; G PROTEIN RECEPTOR FL 2; 1.  
DR PROSITE; PS02622; G PROTEIN RECEPTOR FL 2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Lipoprotein; Palmitate.  
FT DOMAIN 1 19 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 20 40 1 (POTENTIAL).  
FT DOMAIN 41 52 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 53 73 2 (POTENTIAL).  
FT DOMAIN 74 87 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 88 108 3 (POTENTIAL).  
FT DOMAIN 109 131 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 132 152 4 (POTENTIAL).  
FT DOMAIN 153 172 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 173 193 5 (POTENTIAL).  
FT DOMAIN 194 304 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 305 325 6 (POTENTIAL).  
FT DOMAIN 326 341 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 342 362 7 (POTENTIAL).  
FT DOMAIN 363 390 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 87 164 BY SIMILARITY.  
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT LIPID 374 374 S-palmitoyl cysteine (POTENTIAL).  
FT CONFLICT 138 138 A -> V (IN REF. 1).  
FT CONFLICT 206 206 H -> R (IN REF. 1).  
FT CONFLICT 253 253 Q -> R (IN REF. 1).  
SQ SEQUENCE 390 AA; 44495 MW; C986B8AE7FF912C3 CRC64;  
Query Match 66.9%; Score 1370.5; DB 1; Length 390;  
Best Local Similarity 68.1%; Pred. No. 1.2e-85;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
QY 1 MSENSTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDRLNHRSSVFFNLNLAIS 60  
DB 1 MPDNTSTINLSLSTRVTLAFPMFSLVAFAMUGNALVILAFVVDKLNHRSSVFFNLNLAIS 60  
QY 61 DFLVGLISIPLYIPHYLVFNFMNFGSGICMFWLITDYLLCTASVYINVLISYDRYSQSVNAV 120  
DB 61 DFFGVGISIPLYIPHYLVFNFMNFGSGICMFWLITDYLLCTASVYINVLISYDRYSQSVNAV 120  
QY 121 SYRAQHTGIMKIVQMAVAVILAFVNGPMILASDSKNSNTKDCRGFVTEWILIT 180  
DB 121 SYRTQHTGIMKIVQMAVAVILAFVNGPMILASDSKNSNTKDCRGFVTEWILIT 180  
QY 191 MLLEFLLPVI SVAYENVVOIYVSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240  
DB 179 SFLEFVPIVILVAYFNMNIYVSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240  
QY 241 PGLKESAAHSRSESPPRKSSILVSLRTMNSSITAFKVGSPWRSSEALRQREYAEELRG 300  
DB 239 SASTEVPAFSPHQRQRKSSLMFSSRTKMSNTIAKMGFSQSDSVALHQREHVELLRA 298  
QY 301 RKLARSAILLSAFACWAPYCLFTIVLSTYPTPRPKSVWYIAFWLQWNSFVNPPLY 360  
DB 299 RRLAKSLAILLGFAVCAWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPPLY 358  
QY 361 PLCHRRFOKAFWKILCVTKWPAISO-NOSVSS 391  
DB 359 PLCHRRFOKAFWKILCVTKWPAISO-NOSVSS 390  
RESULT 2  
ID HH3R HUMAN STANDARD; PRT; 445 AA.  
AC Q9Y5N1; Q9GZX2; Q9H4K8;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Histamine H3 receptor (HH3R) (G protein-coupled receptor 97).  
GN HHR3 OR GPCR97.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Thalamus;  
 RX MEDLINE=99278519; PubMed=10347254;  
 RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,  
 RA Huvar A., Jackson M.R., Erlander M.G.;  
 RT "Cloning and functional expression of the human histamine H3  
 RT receptor.";  
 RL Mol. Pharmacol. 55:1101-1107(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.  
 RX MEDLINE=20568725; PubMed=11118334;  
 RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;  
 RT "Molecular cloning and characterization of a new human histamine  
 RT receptor, HH4R.";  
 RL Biochem. Biophys. Res. Commun. 279:615-620(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6 AND 7).  
 RC TISSUE=Thalamus;  
 RX MEDLINE=21181559; PubMed=11284713;  
 RA Coge P., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P.,  
 RA Macia C., Ouvre C., Negel N., Rigue H., Boutin J.A., Galizzi J.-P.;  
 RT "Genomic organization and characterization of splice variants of the  
 RT human histamine H3 receptor.";  
 RL Biochem. J. 355:279-288(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME  
 RP VAL-280.  
 RC TISSUE=Blood;  
 RX MEDLINE=21953383; PubMed=11956964;  
 RA Wiedemann P., Boenisch H., Oerters F., Bruess M.;  
 RT "Structure of the human histamine H3 receptor gene (HRH3) and  
 RT identification of naturally occurring variations.";  
 RL J. Neural Transm. 109:443-453(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RP Ullner C., Zirwes E., Lubbert H.;  
 RT "Cloning and functional expression of the human histamine H3  
 RT receptor.";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Lehaeslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).

-!- FUNCTION: The H3 subclass of histamine receptors could mediate the  
 histamine signals in CNS and peripheral nervous system. Signals  
 through the inhibition of adenylylase and displays high  
 constitutive activity (spontaneous activity in the absence of  
 agonist). Agonist stimulation of isoform 3 neither modified  
 adenylylase activity nor induced intracellular calcium  
 mobilization.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=7;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1;  
 CC IsoId=Q9Y5N1-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9Y5N1-2; Sequence=VSP\_001886;  
 CC Name=3; Synonyms=H3S;  
 CC IsoId=Q9Y5N1-3; Sequence=VSP\_001885;  
 CC Name=4;  
 CC IsoId=Q9Y5N1-4; Sequence=VSP\_001881;  
 CC Name=5;  
 CC IsoId=Q9Y5N1-5; Sequence=VSP\_001882;  
 CC Name=6;  
 CC IsoId=Q9Y5N1-6; Sequence=VSP\_001883;  
 CC Name=7;  
 CC IsoId=Q9Y5N1-7; Sequence=VSP\_001884;  
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in the CNS, with the  
 greatest expression in the thalamus and caudate nucleus. The  
 various isoforms are mainly coexpressed in brain, but their  
 relative expression level varies in a region-specific manner.  
 CC Isoforms 3 and 7 are highly expressed in the thalamus, caudate  
 CC nucleus and cerebellum while isoforms 5 and 6 show a poor  
 CC expression. Isoforms 5 and 6 show a high expression in the  
 CC amygdala, substantia nigra, cerebral cortex and hypothalamus.  
 CC Isoform 7 is not found in hypothalamus or substantia nigra.  
 CC -!- DISEASE: Defects in HRH3 are a cause of Shy-Drager syndrome  
 CC [MIM:146500]. This syndrome is characterized by orthostatic  
 CC hypotension, bladder and bowel incontinence, anhidrosis, iris  
 CC atrophy, anisocoria, ataxia, rigidity and tremor.  
 CC -!- MISCELLANEOUS: Does not bind to cimetidine and triptolide. Shows  
 CC modest affinity for thioperamide, imetit, N-alpha-methylhistamine  
 CC and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to  
 CC iodoproxyfan while isoforms 1 and 3 bind it with high affinity.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL; AF140538; AAD38151.1; -  
 CC EMBL; AB045369; BAB20090.1; -  
 CC EMBL; AB019000; BAB7030.1; -  
 CC EMBL; AJ296652; CAC51025.1; -  
 CC EMBL; AJ278250; CAC39434.1; -  
 CC EMBL; AL078633; CAC04014.1; -  
 CC EMBL; AF363791; AAK50040.1; -  
 CC Genbank; HGNC:5184; HRH3.  
 CC MIM; 604525; -  
 CC MIM; 146500; -  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0004969; F:histamine receptor activity; TAS.  
 CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl.; TAS.  
 CC GO; GO:0007269; P:neurotransmitter secretion; TAS.  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC InterPro; IPR003980; H3\_receptor.  
 CC Pfam; PF00001; 7tm1; 1.  
 CC PRINTS; PR00237; GPCR\_Rhodopsn.  
 CC PRINTS; PR01471; HISTAMINEH3R.  
 CC PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 CC PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Alternative splicing; Disease mutation.

FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 40 60 POTENTIAL.

FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 71 91 POTENTIAL.

FT DOMAIN 92 108 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 109 129 POTENTIAL.

FT DOMAIN 130 156 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 157 177 POTENTIAL.

FT DOMAIN 178 196 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 197 217 POTENTIAL.

FT DOMAIN 218 359 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 360 380 POTENTIAL.

FT DOMAIN 381 395 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 396 416 POTENTIAL.

FT DOMAIN 417 445 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 420 23 POLY-ALA.

FT DOMAIN 250 256 POLY-PRO.

FT TRANSSEM 292 298 POLY-GLY.

FT DOMAIN 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT TRANSSEM 85 98 Missing (in isoform 4).

FT TRANSSEM 197 315 Missing (in isoform 5).

FT TRANSSEM 227 342 Missing (in isoform 6).

FT TRANSSEM 234 263 Missing (in isoform 7).

FT TRANSSEM 274 353 Missing (in isoform 3).

FT TRANSSEM 445 445 K > KMKKKTKL (in isoform 2).

FT TRANSSEM 280 280 A -> V (IN SHY-DRAGER SYNDROME).

FT TRANSSEM 19 19 E -> D (IN REF. 1 AND 5).

FT TRANSSEM 445 445 48671 MW; 2ACF7440FBE95B6C CRC64;

FT TRANSSEM 35.3%; Score 722.5; DB 1; Length 445;

FT TRANSSEM 38.8%; Pred. No. 6.5e-42;

FT TRANSSEM 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

FT TRANSSEM 18 LAFLMSSFAFAIMGNVAVILAFVVDRLHRSNYFFLNLAISDFLGLISPLYPHVL 77

FT TRANSSEM 37 LAALMALIVATVLGNLMLAFVADSSLRTQNNFLLNLAISDFLGVACFIPLYPVYL 96

FT TRANSSEM 78 F-NMFGSGICMFWLITDYLLCTASVYINVLISYDRYOSVSNVSYRAQHTGIMKIVQM 136

FT TRANSSEM 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNLVLSYDRFLSVTRAVSYRAQQGDTREAVRM 156

FT TRANSSEM 137 VAVWILAFVNGPMILASDVK-----NSTNTKDCPEGVFTWYILITMLLEFLLPVIS 191

FT TRANSSEM 157 LLLVWVLAFLLYGPAIL---SWELSGGSGSIPGHCYAEFFNYWYFLITASTLEFFTPPLS 213

FT TRANSSEM 192 VAYENVQIY-----WSLWKRLRALSRCPSH 215

FT TRANSSEM 214 VTFNLSIYLNQTRTRLDGAREAGPEPPPEAQPSPPPPGCGWKQKGHEAMPLH 273

FT TRANSSEM 216 -----AGFTSTSSASGHLHRAVACRTSNPGLKSSAASHRESPPRKSILV 263

FT TRANSSEM 274 RYGVGVAAGAEAGATLGGGGG-----GSVASPTSSSG-----SSRGTERPR----- 318

FT TRANSSEM 264 SLRTHMNSSITAFKVSFWRESAALRQ-----EYAEILRGRKLARSILALLSAP 314

FT TRANSSEM 319 -----SLKRGSKPSASASLEKRMKVMVSQFTQRLRDRKVAKSLAVIVSTF 367

FT TRANSSEM 315 AICWAPCYLFTVLSTYPTERKSVYISAFVWLFNSFVNPFLYPLCHRRFQKAFWKI 374

FT TRANSSEM 368 GLCWAPYTLMLIRACHGCHVP-DYWTYSIFWLLWANSVNPVLYPLCHHSFRAFTKL 426

FT TRANSSEM 375 LCVTK 379

FT TRANSSEM 427 LCPQK 431

RESULT 3

HH3R\_CAVPO

ID HH3R\_CAVPO STANDARD; PRT; 445 AA.

AC Q9J135; Q9J136;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 15-MAR-2004 (Rel. 43, Last annotation update)

DE Histamine H3 receptor (HH3R).

GN HH3.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata;

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

OX NCBI\_TaxID=10141;

EN [1]

RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).

RC TISSUE=Brain;

RC MEDLINE=20219440; PubMed=10757514;

RA Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Pillot C.,

RA Cochois V., Schwartz J.-C., Arrang J.-M.;

RA "Cloning and cerebral expression of the guinea pig histamine H3

RT receptor: evidence for two isoforms.";

RL NeuroReport 11:755-759(2000).

CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the

CC histamine signals in CNS and peripheral nervous system. Signals

CC through the inhibition of adenylate cyclase and displays high

CC constitutive activity (spontaneous activity in the absence of

CC agonist).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Long; Synonyms=H3L;

CC IsoId=Q9J135-1; Sequence=Displayed;

CC Name=Short; Synonyms=H3S;

CC IsoId=Q9J135-2; Sequence=VSP\_001880;

CC -!- TISSUE SPECIFICITY: Expressed widely and abundantly throughout the

CC brain. Highly expressed in discrete neuronal populations such as

CC pyramidal cells in cerebral cortex or cerebellar Purkinje cells.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

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CC -----

CC EMBL; AF267537; AAF78947.1; -

DR EMBL; AF267538; AAF78950.1; -

DR InterPro; IPR000276; GPCR\_Rhodpsn.

DR InterPro; IPR003980; H3 receptor.

DR Pfam; PF00001; 7tm\_1; 1

DR PRINTS; PRO0237; GPCRHHODPSN.

DR PRINTS; PRO1471; HISTAMINEH3R.

DR PROSITE; PS00237; G-PROTEIN RECP F1\_1; 1.

DR PROSITE; PS00262; G-PROTEIN RECP F1\_2; 1.

DR G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Alternative splicing.

FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 41 61 POTENTIAL.

FT DOMAIN 62 71 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 72 92 POTENTIAL.

FT DOMAIN 93 109 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 110 130 POTENTIAL.

FT DOMAIN 131 157 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 158 178 POTENTIAL.

FT DOMAIN 179 197 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 198 218 POTENTIAL.

FT DOMAIN 219 359 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 360 380 POTENTIAL.

FT DOMAIN 381 398 EXTRACELLULAR (POTENTIAL).





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RESULT 6
ACM1 MACMU STANDARD; PRT; 460 AA.
ID ACM1 MACMU STANDARD; PRT; 460 AA.
AC P56489;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Muscarinic acetylcholine receptor M1.
GN CHRM1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens epithelium;
RA Rae J.L., Shepard A.R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
CC TURNOVER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF026262; AAB95157.1; -
CC HSP; P02699; IBOV.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
CC Post-synaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Phosphorylation; Multigene family; G-protein coupled receptor.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 47 1 (POTENTIAL).
FT DOMAIN 48 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 82 2 (POTENTIAL).
FT DOMAIN 83 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 121 3 (POTENTIAL).
FT DOMAIN 122 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 164 4 (POTENTIAL).
FT DOMAIN 165 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 209 5 (POTENTIAL).
FT DOMAIN 210 366 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 367 387 6 (POTENTIAL).
FT DOMAIN 388 401 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 402 421 7 (POTENTIAL).
FT DOMAIN 422 460 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 12 12 BY SIMILARITY.
FT DISULFID 98 178 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 428 428 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 451 451 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 455 455 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 457 457 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 460 AA; 51432 MW; 1B19845C3BF79CA CRC64;

Query Match 20.4%; Score 418; DB 1; Length 460;
Best Local Similarity 27.8%; Pred. No. 2.3e-21;
Matches 123; Conservative 83; Mismatches 153; Indels 84; Gaps 19;
OY 5 NSTGLPPAAQVPLAFL---MSSFAFAIMGVNAVILAFVVDRLNLRHSNYFFFLNLAISD 61

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Db 12 NITVLAPGKGPQVAFIGITITGLLSATVTGNLLVLSFKVTELTKNVNFLLSLACD 71
QY 62 FLVGLISIPYIPIHVLIF-NWNFSGGICMFWLLITDYLLCTASVYNIVLISDYQSVNAV 120
Db 72 LIIGTFSMNLTYTLLMHWALGTACDLWLALDYVASNASVNNLLISFDYFVSFTRPL 131
QY 121 SYRAOHTGIMKIVAOVAV-WILAFVNGPMILASDSWKNSTWK-----DCPPGFVTEW 174
Db 132 SYRAKET--PRAALMIGLAWLWFLWAPAIL---FWQYLVGERTVLGAGCCYIQFLSQP 186
QY 175 YLITIMLLLEFLLPVISVAYENVQIYWSLWKR-----RAL-----SRCPSHAGFTSS- 223
Db 187 IITFGTAAAFYLPVTVMC-----TLIWRIYRETNARELAALQSGETPKGGGGSSSE 242
QY 224 ----SASGHLHR-AGVACRTSNP-----GLKESAARHSESFRKSSI 261
Db 243 RSQPGAEGSPETPPGRCRCRPPRLQAYSWKEDDEEGSMESLTSSEGEFP--GSEV 300
QY 262 LVSL-----RTHNSSITAFKVGFWRSESA-----ALKQRYAEL 297
Db 301 VIKMPMVDPEAAPTQKPPRSPENTVKRPTKG---RDRAGKQKPRGKQLAKRTFSL 357
QY 298 LRGRKLARSILAILLSAPAIWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLWENFSFVNP 357
Db 358 VREKKAARTLSALLAFILTWPTNIMLV-STFCXCVPEILW-ELGWLVCYNSTINP 415
QY 358 FLYPLCHRRFPQKAFKILCVTKW 380
Db 416 MCVALCNKAFRDTF-RLLLLCRW 437

RESULT 7
ACM5 MACMU STANDARD; PRT; 532 AA.
ID ACM5 MACMU STANDARD; PRT; 532 AA.
AC P56490;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Muscarinic acetylcholine receptor M5.
GN CHRM5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens epithelium;
RA Rae J.L., Shepard A.R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
CC TURNOVER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC -----
CC EMBL; AF026264; AAB95159.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.

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OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RT [1]  
RP SEQUENCE FROM N.A.  
RP MEDLINE=88096607; PubMed=3697105;  
RA Allard W.J., Sigal I.S., Dixon R.A.F.;  
RT "sequence of the gene encoding the human M1 muscarinic acetylcholine  
RT receptor.";  
RL Nucleic Acids Res. 15:10604-10604(1987).  
RL [2]  
RP SEQUENCE FROM N.A.  
RP MEDLINE=90245684; PubMed=2336407;  
RA Chapman C.G., Browne M.J.;  
RT "Isolation of the human m1 (Hml) muscarinic acetylcholine receptor  
RT gene by PCR amplification.";  
RL Nucleic Acids Res. 18:2191-2191 (1990).  
RL [3]  
RP SEQUENCE FROM N.A.  
RP MEDLINE=88166632; PubMed=3443095;  
RA Peralta E.G., Ashkenazi A., Winslow J.W., Smith D.H.,  
RA Ramachandran J., Capon D.J.;  
RT "Distinct primary structures, ligand-binding properties and tissue-  
RT specific expression of four human muscarinic acetylcholine  
RT receptors.";  
RL EMBO J. 6:3923-3929 (1987).  
RL [4]  
RP SEQUENCE FROM N.A.  
RP TISSUE=Brain;  
RC Puhl H.B. III, Ikeda S.R., Aronstam R.S.;  
RT "cDNA clones of the human proteins involved in signal transduction  
RT sequenced by the Guthrie cDNA resource center ([www.cdna.org](http://www.cdna.org)).";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RL [5]  
RP SEQUENCE FROM N.A.  
RP TISSUE=Brain;  
RC MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Scherz T.E.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
RA Butterfield Y.S.N., Krzyzyski M.I., Skaleka U., Smallus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RL [6]  
RP MUTAGENESIS.  
RP MEDLINE=93075202; PubMed=1445347;  
RA Arden J.R., Nagata O., Shockley M.S., Philip M., Lameh J., Sadee W.,  
RT "Mutational analysis of third cytoplasmic loop domains in G-protein  
RT coupling of the Hm1 muscarinic receptor.";  
RL Biochem. Biophys. Res. Commun. 188:1111-1115 (1992).  
CC -1- FUNCTION: The muscarinic acetylcholine receptor mediates various  
CC cellular responses, including inhibition of adenylate cyclase,  
CC breakdown of phosphoinositides and modulation of potassium  
CC channels through the action of G proteins. Primary transducing  
CC effect is PI turnover.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.



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EMBL	X52068	CAA36291.1	-	
DR	DR	DR	DR	DR
EMBL	X15263	CAA33334.1	-	
DR	DR	DR	DR	DR
EMBL	Y00508	CAA68560.1	-	
DR	DR	DR	DR	DR
EMBL	AF498915	AAM18938.1	-	
DR	DR	DR	DR	DR
EMBL	BC007740	AAHG7740.1	-	
DR	DR	DR	DR	DR
EMBL	BC022984	AAH22984.1	-	
DR	DR	DR	DR	DR
PIR	S09508	S09508		
DR	DR	DR	DR	DR
HSSP	P02699	1BOJ		
DR	DR	DR	DR	DR
Genew	HGNC:1950	CHRM1		
DR	DR	DR	DR	DR
MIM	118510	-		
DR	DR	DR	DR	DR
GO	GO:0005887	C:integral to plasma membrane	TAS.	
DR	DR	DR	DR	DR
GO	GO:0005624	C:membrane fraction	TAS.	
DR	DR	DR	DR	DR
GO	GO:0004981	F:muscarinic acetylcholine receptor activity	TAS.	
DR	DR	DR	DR	DR
GO	GO:0007213	P:acetyl choline receptor signaling, muscarin. . .	TAS.	
DR	DR	DR	DR	DR
GO	GO:0008283	P:cell proliferation	TAS.	
DR	DR	DR	DR	DR
GO	GO:0007207	F:muscarinic acetyl choline receptor, phospho. . .	TAS.	
DR	DR	DR	DR	DR
GO	GO:0007399	P:neurogenesis	TAS.	
DR	DR	DR	DR	DR
GO	GO:0007203	P:phosphatidylinositol-4,5-bisphosphate hydro. . .	TAS.	
DR	DR	DR	DR	DR
GO	GO:0008284	P:positive regulation of cell proliferation	TAS.	
DR	DR	DR	DR	DR
GO	GO:0007205	P:protein kinase C activation	TAS.	
DR	DR	DR	DR	DR
GO	GO:0006474	P:protein modification	TAS.	
DR	DR	DR	DR	DR
GO	GO:0007165	P:signal transduction	TAS.	
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InterPro	IPR000276	GPCR_Rhodpsn		
DR	DR	DR	DR	DR
Pfam	PF00001	7tm_1		
DR	DR	DR	DR	DR
PRINTS	PR00237	GECRRHODPSN		
DR	DR	DR	DR	DR
PROSITE	PS00237	G PROTEIN RECP F1.1	1.	
DR	DR	DR	DR	DR
PROSITE	PS50262	G PROTEIN RECP F1.2	1.	
DR	DR	DR	DR	DR
KW	Postsynaptic membrane	Ionic channel	Glycoprotein	Transmembrane
DR	DR	DR	DR	DR
KW	Phosphorylation	Multigene family	G-protein coupled receptor	
DR	DR	DR	DR	DR
FT	DOMAIN	1	24	EXTRACELLULAR (POTENTIAL)
FT	TRANSMEM	25	47	1 (POTENTIAL)
FT	DOMAIN	48	61	CYTOPLASMIC (POTENTIAL)
FT	TRANSMEM	62	82	2 (POTENTIAL)
FT	DOMAIN	83	99	EXTRACELLULAR (POTENTIAL)
FT	TRANSMEM	100	121	3 (POTENTIAL)
FT	DOMAIN	122	141	CYTOPLASMIC (POTENTIAL)
FT	TRANSMEM	142	164	4 (POTENTIAL)
FT	DOMAIN	165	186	EXTRACELLULAR (POTENTIAL)
FT	TRANSMEM	187	209	5 (POTENTIAL)
FT	DOMAIN	210	366	CYTOPLASMIC (POTENTIAL)
FT	TRANSMEM	367	387	6 (POTENTIAL)
FT	DOMAIN	388	401	EXTRACELLULAR (POTENTIAL)
FT	TRANSMEM	402	421	7 (POTENTIAL)
FT	DOMAIN	422	460	CYTOPLASMIC (POTENTIAL)
FT	CARBOHYD	2	2	N-LINKED (GLCNAC. . .) (PROBABLE)
FT	CARBOHYD	12	12	N-LINKED (GLCNAC. . .) (PROBABLE)
FT	DISULFID	98	178	BY SIMILARITY
FT	MOD_RES	428	428	PHOSPHORYLATION (POTENTIAL)
FT	MOD_RES	451	451	PHOSPHORYLATION (POTENTIAL)
FT	MOD_RES	455	455	PHOSPHORYLATION (POTENTIAL)
FT	MOD_RES	457	457	PHOSPHORYLATION (POTENTIAL)
FT	CONFLICT	173	173	V -> M (IN REF. 3)
DR	DR	DR	DR	DR
SEQUENCE	460 AA	51420 MW	567C20F63541C8D0	CRG64

Query Match	20.2%;	Score 413;	DB 1;	Length 460;
Best Local Similarity	27.4%;	Pred. No. 4.9e-21;		
Matches 122;	Conservative 84;	Mismatches 150;	Indels 90;	Gaps 19;
QY	5	NSTGILPPAAQVPLAE	-----MGSFAPAIMGVNAVILAFVVDRLNLRHSRNYFFLNLAISD	61
Db	12	NITVLAPGRGPQVAFIGITIGLSLATVGTGNLLVLIISPKVNTKLVNNYELLSIACAD	71	
QY	62	FVAGLJISIPLYIPHLVFNWNGSGICMPWLITDYLCTASTVYNIVLISDRIYQSVNAV	120	
Db	72	LIIGTFSMNLTYLLMGHWALGTACDLMALDXYVNASNMVNLILSTFDRIYFSVTRPL	131	

QY	121	SYRAQHTGIMKIVAQMVAV-WILAPLVNPNMILASDSWKNSNTXK-----DCEPQGVFTW	178
DB	132	SYRAKT--PRAALMIGLAWLSVFLWAPAIL---FWQYLVGERTVLGAGQVYQFLSQP	186
QY	175	YLITITMLLELLPVISVAYENVQIYWSLWR-----RAL-----SRCPSHAGFTTSS	224
DB	187	IITGTAWAAYLPVTVMC-----TLYMRYIRETENARELAALQOSETPGKGGSSSSSE	242
QY	225	AS-----CHLHRAGVACRT-----SNPGLKESAASHSESPPRK	258
DB	243	RSQPGAEGSPETPGRCR---CCRAPELLOAYSWEKEEEDGSWESLTSSEGP--G	297
QY	259	SSILVSL-----RTHMNSSITAFKVGSWRSESA-----ALRQREY	294
DB	298	SEVVIKPMVMDPEAQAPTKPPRSPNTVKRPTKKG---RDRAGKQKPRGKEQLAKRKT	354
QY	295	AELLRGKRLARSIALISAPALCWAPYCLFTIVLSTYPTERTPRKSVWYSIAFWLOWNSF	354
DB	355	FSLVKEKAARTLSAIIAFLITWTPYNIWIV-STFCCKQVPETLW-ELGWLCYVNST	412
QY	355	VNPLYPLCHRRFQKAFWKILCVTKW	380
DB	413	INPCYALCNKAFRDTF-RLLLCRW	437
RESULT 9			
ACMI_PIG	ACM1_PIG	STANDARD;	PRT; 460 AA.
ID	AD	P04761;	
DT	DT	13-AUG-1987 (Rel. 05, Created)	
DT	DT	13-AUG-1987 (Rel. 05, Last sequence update)	
DT	DT	16-OCT-2001 (Rel. 40, Last annotation update)	
GN	GN	Muscarinic acetylcholine receptor M1.	
DE	DE	CHRM1.	
OS	OS	Sus scrofa (Pig).	
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OX	OX	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
NCBI_TaxID=9623;	NCBI_TaxID=9623;		
[1]	[1]		
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.		
TISSUE=Brain;	TISSUE=Brain;		
MEDLINE=87014801; PubMed=3762692;	MEDLINE=87014801; PubMed=3762692;		
Kubo T., Fukuda K., Mikami A., Maeda A., Takahashi H., Mishina M.,	Kubo T., Fukuda K., Mikami A., Maeda A., Takahashi H., Mishina M.,		
Haga T., Haga K., Ichiyama A., Kangawa K., Kojima M., Matsuo H.,	Haga T., Haga K., Ichiyama A., Kangawa K., Kojima M., Matsuo H.,		
Harose T., Numa S.;	Harose T., Numa S.;		
"Cloning, sequencing and expression of complementary DNA encoding the	"Cloning, sequencing and expression of complementary DNA encoding the		
muscarinic acetylcholine receptor."	muscarinic acetylcholine receptor."		
Nature 323:411-416(1986).	Nature 323:411-416(1986).		
- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS	- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS		
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,	CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,		
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS	BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS		
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI	THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI		
TURNOVER.	TURNOVER.		
- SUBCELLULAR LOCATION: Integral membrane protein.	- SUBCELLULAR LOCATION: Integral membrane protein.		
- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.		
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or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
EMBL; X04413; CAA28003.1; -.	EMBL; X04413; CAA28003.1; -.		
PIR; A24325; A24325.	PIR; A24325; A24325.		
HSSP; P02699; 1BQJ.	HSSP; P02699; 1BQJ.		
InterPro; IPR000276; GPCR_Rhodpsn.	InterPro; IPR000276; GPCR_Rhodpsn.		
Efam; PF00001; 7tm 1; 1.	Efam; PF00001; 7tm 1; 1.		
PRINTS; PR00237; GPCRHHODPSN.	PRINTS; PR00237; GPCRHHODPSN.		
PROSITE; PS00237; G PROTEIN RECEPT F1; 1.	PROSITE; PS00237; G PROTEIN RECEPT F1; 1.		
PROSITE; PS00262; G PROTEIN RECEPT F1-2; 1.	PROSITE; PS00262; G PROTEIN RECEPT F1-2; 1.		

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KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Phosphorylation; Multigene family; G-protein coupled receptor.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 47 1 (POTENTIAL).
FT DOMAIN 48 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 82 2 (POTENTIAL).
FT DOMAIN 83 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 121 3 (POTENTIAL).
FT DOMAIN 122 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 164 4 (POTENTIAL).
FT DOMAIN 165 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 209 5 (POTENTIAL).
FT DOMAIN 210 366 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 367 387 6 (POTENTIAL).
FT DOMAIN 388 401 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 402 421 7 (POTENTIAL).
FT DOMAIN 422 460 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (PROBABLE).
FT DISULFID 12 12 BY SIMILARITY.
FT MOD RES 428 428 PHOSPHORYLATION (POTENTIAL).
FT MOD RES 451 451 PHOSPHORYLATION (POTENTIAL).
FT MOD RES 455 455 PHOSPHORYLATION (POTENTIAL).
FT MOD RES 457 457 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 460 AA; 51418 MW; C025C70EA43BC2AD CRC64;

Query Match 20.2%; Score 413; DB 1; Length 460;
Best Local Similarity 27.5%; Pred. No. 4.9e-21;
Matches 122; Conservative 83; Mismatches 154; Indels 84; Gaps 18;

QY 5 NSTGILPPAAQVPLAFL--MSSFAFALMGVNAVILAFVVDRLNLRHRSNYFFFLNLAISD 61
DB 12 NITVLAPGKGWQVAFGIITGLISLATVGNLLVILISFKVNTLKTNNYFLSLACAD 71

QY 62 FLVGLISIPYIHPVLP-NMNFSGICMFWLITDYLLCTASVYINVLISDYRQSVNAV 120
DB 72 LIIGTFSMNLYTTLVLMGHWALGTIIGLLSLATVGNLLVILISFKVNTLKTNNYFLSLACAD 71

QY 121 SYRAQHTGIMKIVQAVAV-WILAFVNGPMLASDSWKNSTNTK-----DCEPGFVTEM 174
DB 132 SYRAKRT--PRAALMIGLAWLVSVLWAPAIL---FWQYIVGERTVLAGQCYQLFSLQP 186

QY 175 YILITLMLLELLPVISVAYENVQVLSLWKR-----RAL-----SRCFSGHAGSTTSSS 224
DB 187 IITFGTAAAPYLPVTVMC-----TLYWKLYRETNARELAALQGETPGKGGSSSSSE 242

QY 225 AS-----GHLHRAGVACT-----SNPGLKESAAGRHSSEPRK 258
DB 243 RSQPGAEGSPETPPGCCR---CCRAPRLQAYSWKBEEDEGSMESLTSSEGEPE--G 297

QY 259 SSILVSL-----RTHMNSSITAFKVGSWRSAA-----LRQREYABL 297
DB 298 SEVVIKMPWVDEAQAQAPKQPPRPSPNTVKRGRBRAGKQKPKQKAKRTFSL 357

QY 298 LRGRKLARSALLSAFAICWAPYCLFTITVSTYPRTPKPSVWYSIAFWLQWNSFVNP 357
DB 358 VKEKAARTLSAILAFIVTWPYINVLV-STFCKDCVPEFLM-ELGWYLCVYNSTNP 415

QY 358 FLYPLCHRRFQKAFKWLICVTKW 380
DB 416 MCYALCNKAFRTDF-RLLLLCRW 437

RESULT 10
ACM5_RAT
ID ACM5_RAT STANDARD; PRT; 531 AA.
AC P08311;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Muscarinic acetylcholine receptor M5.
GN CHRM5 OR CHRM-5.
OS Rattus norvegicus (Rat).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90166521; PubMed=3272174;
RA Bonner T.I., Young A.C., Brann M.R., Buckley N.J.;
RT "Cloning and expression of the human and rat m5 muscarinic
RT acetylcholine receptor genes.";
RL Neuron 1:403-410(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89214170; PubMed=2540186;
RA Liao C.-F., Themmen A.P.N., Joho R., Barberis C., Birnbaumer M.,
RA Birnbaumer L.;
RT "Molecular cloning and expression of a fifth muscarinic acetylcholine
RT receptor.";
RL J. Biol. Chem. 264:7328-7337(1989).
CC -1- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
CC TURNOVER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
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EMBL; M22926; AAA40658.1; -
EMBL; M22925; AAA41572.1; -
PIR; JT0531; JT0531.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCR_Rhodopsin.
PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECP_F2_1; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
Phosphorylation; Multigene family; G-protein coupled receptor.
KW DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 29 52 1 (POTENTIAL).
FT DOMAIN 53 65 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 66 86 2 (POTENTIAL).
FT DOMAIN 87 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 125 3 (POTENTIAL).
FT DOMAIN 126 145 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 146 168 4 (POTENTIAL).
FT DOMAIN 169 190 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 191 213 5 (POTENTIAL).
FT DOMAIN 214 442 6 (POTENTIAL).
FT TRANSMEM 443 463 7 (POTENTIAL).
FT DOMAIN 464 477 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 478 497 7 (POTENTIAL).
FT DOMAIN 498 531 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 102 182 BY SIMILARITY.
FT MOD RES 500 500 PHOSPHORYLATION (POTENTIAL).
FT MOD RES 504 504 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 531 AA; 60136 MW; 647CE0D5D75A2BB1 CRC64;

Query Match 20.0%; Score 410.5; DB 1; Length 531;
Best Local Similarity 24.6%; Pred. No. 8.3e-21;
Matches 122; Conservative 92; Mismatches 140; Indels 141; Gaps 15;

QY 16 VPLAFIMSSFAFALMGVNAVILAFVVDRLNLRHRSNYFFFLNLAISDFLVGLISIPYIHP 75
DB 30 ITIAVTVAVSLMTIVGNVLMVWISFKVNSQLKTVNNYLLSLACADLIIGFMSNLYTTY 89
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QY 76 VLF-NWFGSGICMFWLITDYLCTASVYNIIVLSIDRYQSVNAVSYRAQHT-----GIM 130
Db 90 ILMGKRWLGLSLADLWDVAGSNVWMLLVISDFRYFSITRPLTYRAKSTPKRAGIM 149
QY 131 KIVAQWAVVLLAFVNGPMLASDSW-----KNSWTYKCEPGFVTEWYILTTIMLLEF 185
Db 150 IGLA-----WLVSLWAPAILC---WQYLVGKRTVPPDECIQFLSEPTITFGTAIAAF 201
QY 186 LLPVISVAYFNQIYWSLWKR-----RALSRCP----- 213
Db 202 YIPVSWTILYCRYRTERKTKDLADLQSDSVABAKKREPAORTLLRSFFSPRSLA 261
QY 214 -----SHAGFSTT---SSASGHLHRA-----GVACRTSNPGLKESA----- 247
Db 262 QRENOASWSSRRSTSTGTGTTQATDLADWEKAEQVTTCSYPSSEDEAKPTTDPVFO 321
QY 248 ---ASRHSSEPRKSSILVSLRTHMSSI---TAFKVGSEFWSESAALR----- 290
Db 322 MVYSEAKESPGKESNTQETKTVNTRTENSDDYTPKFLSPAAHRLKSQKCVAYKFR 381
QY 291 -----OREYAEALLRGRKLAR 305
Db 382 LVVKADGTQETNNGCRVKIMPCSPFVSKDPSTKGPDPNLSHQWTKRKMVLVKERKAAQ 441
QY 306 SLAILLSAFAICWAPYCLFIVLSTYRTERPKSVWYVSIAPFQWENSVFNPFLYPLCHR 365
Db 442 TLSAILLAFTITWTPYNIWLV-STFCDCKCPVTLWH-LGWLCYVNSTINPICYALCNR 499
QY 366 RFQKAFWKILCVTKM 380
Db 500 TFRKTF-KLULLCRW 513

RESULT 11
ACM3_PIG
ID ACM3_PIG STANDARD; PRT; 590 AA.
AC FILL483;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Muscarinic acetylcholine receptor M3.
GN CHRM3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296835; PubMed=3402600;
RA Akiba I., Kubo T., Maeda A., Bujo H., Nakai J., Mishina M., Numa S.;
RT "Primary structure of porcine muscarinic acetylcholine receptor III
RT and antagonist binding studies.";
RL FEBS Lett. 235:257-261(1988).
CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
CC TURNOVER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X12712; CAA31215.1; -
CC PIR; S01114; S01114.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
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DR PRINTS; PR00237; GPCRHOPOSN
DR PROSITE; PS00237; G-PROTEIN RECEPT F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPT F1_2; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Phosphorylation; Multigene family; G-protein coupled receptor.
FT DOMAIN 1 67
FT TRANSMEM 68 91
FT DOMAIN 92 104
FT TRANSMEM 105 125
FT DOMAIN 126 142
FT TRANSMEM 143 164
FT DOMAIN 165 184
FT TRANSMEM 185 207
FT DOMAIN 208 229
FT TRANSMEM 230 252
FT DOMAIN 253 492
FT TRANSMEM 493 513
FT DOMAIN 514 527
FT TRANSMEM 528 547
FT DOMAIN 548 590
FT CARBOHYD 6 6
FT CARBOHYD 7 7
FT CARBOHYD 8 8
FT CARBOHYD 15 15
FT CARBOHYD 41 41
FT CARBOHYD 48 48
FT CARBOHYD 53 53
FT DISULFID 141 221
SQ SEQUENCE 590 AA; 66077 MW; 9998D2A4802FD32A CRC64;

Query Match 20.0%; Score 410.5; DB 1; Length 590;
Best Local Similarity 24.8%; Pred. No. 9.1e-21;
Matches 125; Conservative 82; Mismatches 136; Indels 161; Gaps 16;

QY 18 LAFELMSFAFIMVGNVAVILAFVDRNLRHRSNYFFFLNALISDELVGLISIPLYPHVL 77
Db 71 IAEFTGILALVTIIGNIVLIVAFKVNKQKTVNNYFLLSLACADLLIGVISMLFTYII 130
QY 78 FN-WNFGSGICMFWLITDYLCTASVYNIIVLSIDRYQSVNAVSYRAQHT-----GIMKI 132
Db 131 MNRWALGNLACDLWLSIDYVNASVMNLLVISDFRYFSITRPLTYRAKSTPKRAGVMIG 190
QY 133 VQWQWAVVLLAFVNGPMLASDSWKNSTNTKDCBPG-----FVTEWYILTTIMLLEFL 187
Db 191 LA-----WVLSFILWAPAIL---FWQYFVGKRTVPPEGECFIQFLSEPTITFGTAIAAFYM 242
QY 188 PVISVAYFNQIYWSLWKRRLSRCPSHAGF---STTSSASGHLHRAAGVACRTSNPGLKE 245
Db 243 PVTIMTI---LYWRIYKETE-KRYKELAGLQASGTEAEAEFVHPTGSSRSCSYELOQ 297
QY 246 SAASR-----HSES----- 254
Db 298 QSLKRSARKYGRCHFWFTTKWKPSEAQMDQDSSSDSMNNNDAAASLENSASSDEEDI 357
QY 255 ---PRKKSILVSLRTHM-----SSITAFKV----- 278
Db 358 GSETAIYSIVLKLPGHSTILNSTKLPSDNLQVPEELGTVDLERKASKLOAQKMDDG 417
QY 279 GSFWR-----ESAA-----LRQ 291
Db 418 GSFQKSFSLPIQLESADVDTAKASDVNSVSGKTTATLPLSFKEATLAKRFAUKTRSQITK 477
QY 292 REYABELRGRKLARSLAILLSAFAICWAPYCLFIVLSTYRTERPKSVWYVSIAPFQW 351
Db 478 RKRMSLIKEAKAAQTLSSAILLAFTITWTPYNIWLV-NTFDCSCPDKTYW-NLGYWLCYI 535
QY 352 NSFVNPFYPLCHRRPQKAFWKIL 375
Db 536 NSTVNPVCYALCNKTKTFTTFRKML 559

RESULT 12
ACM1_RAT
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ID AC01 RAT STANDARD; PRT; 450 AA.  
 AC P08482;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, last sequence update)  
 DT 28-FEB-2003 (Rel. 41, last annotation update)  
 DE Muscarinic acetylcholine receptor M1.  
 GN CHRM1 OR CHRM-1  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=87263421; PubMed=3037705;  
 RA Bonner T.I., Buckley N.J., Young A.C., Brann M.R.;  
 RA "Identification of a family of muscarinic acetylcholine receptor  
 RT genes.";  
 RL Science 237:527-532 (1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=92101806; PubMed=1759615;  
 RA Lai J., Smith T.B., Mei L., Ikeda M., Fujiwara Y., Gomez J.,  
 RA Halonen M., Roeseke W.R., Yamamura H.I.;  
 RA "The molecular properties of the M1 muscarinic receptor and its  
 RT regulation of cytosolic calcium in a eukaryotic gene expression  
 RT system.";  
 RL Adv. Exp. Med. Biol. 287:313-330 (1991).  
 RN [3]  
 RP MUTAGENESIS OF CYSTEINE RESIDUES.  
 RP MEDLINE=92283857; PubMed=1317867;  
 RA Savarese T.M., Wang C.-D., Fraser C.M.;  
 RA "Site-directed mutagenesis of the rat M1 muscarinic acetylcholine  
 RT receptor. Role of conserved cysteines in receptor function.";  
 RL J. Biol. Chem. 267:11439-11448 (1992).  
 CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS  
 CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,  
 CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS  
 CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI  
 CC TURNOVER.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL; M16406; AAA00660.1; -;  
 CC EMBL; S73971; AAB20705.1; -;  
 CC PIR; A94518; A29514.  
 CC HSP; P02699; IBOU.  
 CC InterPro; IPR000276; GPCR\_Rhodpsn.  
 CC Pfam; PF00001; 7tm 1; 1.  
 CC PRINTS; PR00237; GPCRHOPOSN.  
 CC PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 CC PROSITE; PS00262; G-PROTEIN RECP\_F1\_2; 1.  
 CC Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;  
 KW Phosphorylation; Multigene family; G-protein coupled receptor.  
 FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 25 47 1 (POTENTIAL).  
 FT DOMAIN 48 61 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 62 82 2 (POTENTIAL).  
 FT DOMAIN 83 99 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 100 121 3 (POTENTIAL).  
 FT DOMAIN 122 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 164 4 (POTENTIAL).  
 FT DOMAIN 165 186 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 187 209 5 (POTENTIAL).  
 FT DOMAIN 210 366 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 367 387 6 (POTENTIAL).

FT DOMAIN 388 401 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 402 421 7 (POTENTIAL).  
 FT DOMAIN 422 460 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (PROBABLE).  
 FT CARBOHYD 12 12 N-LINKED (GLCNAC. . .) (PROBABLE).  
 FT DISULFID 98 178 PROBABLE.  
 FT MOD RES 428 451 PHOSPHORYLATION (POTENTIAL).  
 FT MOD RES 451 451 PHOSPHORYLATION (POTENTIAL).  
 FT MOD RES 457 457 PHOSPHORYLATION (POTENTIAL).  
 SQ SEQUENCE 460 AA; 51368 MW; 527573ED8FF7C317 CRC64;  
 Query Match 20.0%; Score 410; DB 1; Length 460;  
 Best Local Similarity 27.4%; Pred. No. 7.8e-21;  
 Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;  
 QY 5 NSTGILPPAAQVPLAFL---MSSFAFAIMVGNVAVILAVVVDRLRLRSNYFFFLNLAISD 61  
 DB 12 NITVLAFGKGPWQVAFIGITGLLSLATVGNLVLISFKVNTKVTNNYFLLSLACAD 71  
 QY 62 FLVGLISITPLYPHVLF-NWNFGSGICFMFLITDYLCTASVYVIVLISYDYSVSNV 120  
 DB 72 LIIGTFSNLYTYLLMGHMGALGTACDLWLALDYVASNAGVNMILLISFDRIYSVTRPL 131  
 QY 121 SYRAQHTGIMKIVQMVAV-WILAFVNGPMLASDSWKNSTNYK-----DCEPGFVTEW 174  
 DB 132 SYRAKRT--PRRAALMIGLAWLVSVFLWAPAIL---FMQYLVGERTVLAGCYIQFLSOP 186  
 QY 175 YLITITMLLEFLPLVISVAYENVVOIYNSLWKR-----RAL-----SRCPSHAGFTTSSS 224  
 DB 187 IITGTAAFAFLPVTVNMC-----TLWRIYRETNARELAALQGSFPGKGGSSSSE 242  
 QY 225 AS-----GHLHRAGVACRT-----SNPGLKESAAHSHSSPRRK 258  
 DB 243 RSQPAEGSPSPGRCR---CCRAPLLQAYSWEKEEEDSGMSLTSSEGESE--G 297  
 QY 259 SSILVSL-----RTHMNSITAFKVGSPWSESA-----ALRQREY 294  
 DB 298 SEVWIKMPWVDSQAQPTKQPPKSPNTVKRPTKKG---RDRGGKQKPRGKEQLAKRKT 354  
 QY 295 AELLGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSF 354  
 DB 355 FSLVKEKKAARLSAILLAFLITWTPYINMVLV-STFKDCVCPETLM-ELGYWLCYVNST 412  
 QY 355 VNPFLYPLCHRRFQKAFWKILCVTKW 380  
 DB 413 VNPMCYALCNKAFRDTF-RLLLLCRW 437  
 RESULT 13  
 ACM3 BOVIN STANDARD; PRT; 590 AA.  
 AC P41984;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, last sequence update)  
 DT 15-MAR-2004 (Rel. 43, last annotation update)  
 DE Muscarinic acetylcholine receptor M3.  
 GN CHRM3.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Brain;  
 RC MEDLINE=94339178; PubMed=8061048;  
 RA Lee P.H., Hodges P.K., Glickman F., Chang K.J.;  
 RA "Cloning and expression of a cDNA encoding bovine muscarinic  
 RT acetylcholine m3 receptor.";  
 RL Biochim. Biophys. Acta 1223:151-154 (1994).  
 RN [2]  
 RP SEQUENCE OF 327-467 FROM N.A.







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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:06:02 ; Search time 44 Seconds  
(without alignments)  
2803.809 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mmc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_virus.\*

16: sp\_bacterioph.\*

17: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2035	99.4	391	11 Q91ZY2	Q91zy2 mus musculus
2	1745	85.2	391	11 Q91ZY1	Q91zy1 rattus norv
3	1372.5	67.0	390	4 Q96LD9	Q96ld9 homo sapien
4	1311.5	64.0	390	6 Q8MNV9	Q8mrv9 sus scrofa
5	1238	60.4	389	11 Q91ZY3	Q91zy3 cavia porce
6	718.5	35.1	445	6 Q865E1	Q865el macaca mula
7	665.5	32.5	365	4 Q8WY01	Q8wy01 homo sapien
8	665.5	32.5	373	4 Q8WY01	Q8wy01 homo sapien
9	492.5	24.0	301	4 Q8WY00	Q8wxz9 homo sapien
10	492.5	24.0	309	4 Q8WY00	Q8wy00 homo sapien
11	415.5	20.3	530	11 Q8VH24	Q8vhl24 cavia porce
12	413	20.2	454	4 Q96RH1	Q96rhl1 homo sapien
13	410	20.0	460	11 Q8BJN3	Q8bjn3 mus musculus
14	410	20.0	587	11 Q8VH26	Q8vhw26 cavia porce
15	406.5	19.8	532	4 Q81VW0	Q81vw0 homo sapien
16	406	19.8	490	13 Q7T286	Q7t286 brachydanio

17	405.5	19.8	200	4 Q8NI50	Q8ni50 homo sapien
18	405	19.8	458	11 Q8VH28	Q8vh28 cavia porce
19	402.5	19.7	564	4 Q96RG9	Q96rg9 homo sapien
20	401.5	19.6	528	13 Q9PTF6	Q9ptf6 gallus gall
21	401.5	19.6	532	11 Q920H4	Q920h4 mus musculus
22	393.5	19.2	518	6 Q9MYI8	Q9myi8 oryctolagus
23	392.5	19.2	400	6 Q8MKJ0	Q8mkj0 cebus apell
24	391	19.1	488	11 Q91V49	Q91v49 rattus norv
25	390.5	19.1	147	6 Q865E3	Q865e3 canis famil
26	390	19.0	571	6 Q9TWM9	Q9ttm9 sus scrofa
27	389.5	19.0	459	11 Q8CGI5	Q8cgl5 mus musculus
28	389.5	19.0	487	6 Q9N2B1	Q9n2b1 gorilla gor
29	389.5	19.0	487	6 Q9N2B0	Q9n2b0 pongo pygma
30	389.5	19.0	515	11 Q9DBL0	Q9db10 mus musculus
31	389	19.0	488	11 Q91V66	Q91v66 rattus norv
32	388.5	19.0	495	13 Q801M4	Q801m4 brachydanio
33	386.5	18.9	487	6 Q9N2B2	Q9n2b2 pan troglod
34	384.5	18.8	399	5 Q9NG02	Q9ng02 apis mellif
35	384	18.8	477	11 Q8VH25	Q8vh25 cavia porce
36	383.5	18.7	559	11 Q9QW71	Q9qw71 rattus sp.
37	382.5	18.7	466	11 Q8VH27	Q8vh27 cavia porce
38	382	18.7	399	4 Q13167	Q13167 homo sapien
39	382	18.7	474	4 Q96RG8	Q96rg8 homo sapien
40	381	18.6	415	13 Q8JG69	Q8jg69 brachydanio
41	380.5	18.6	456	4 Q96RH0	Q96rh0 homo sapien
42	380.5	18.6	506	5 Q8IS44	Q8is44 drosophila
43	378	18.5	461	5 Q8IS43	Q8is43 drosophila
44	376.5	18.4	410	5 Q86GT6	Q86gt6 caenorhabdi
45	376.5	18.4	422	5 Q8T3C1	Q8t3c1 caenorhabdi

## ALIGNMENTS

### RESULT 1

Q91ZY2 ID Q91ZY2 PRELIMINARY; PRT; 391 AA.  
AC Q91ZY2;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Histamine H4 receptor.  
GN HRR4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/c;  
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
RT "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor  
RT suggests substantial species variation."  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AF358859; AAK97380.1; -;  
DR MGD; MGI:2429635; Hrh4.  
DR GO; GO:0005887; C:Integral to plasma membrane; IC.  
DR GO; GO:0005624; C:membrane fraction; IDA.  
DR GO; GO:0004969; F:histamine receptor activity; IDA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR008102; Histamine\_H4.  
DR Pfam; PF00001; 7tm1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsin.  
DR PRINTS; PR01726; HISTAMINEH4.  
DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS00362; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 391 AA; 44248 MW; 59EC73CB5214C5E0 CRC64;  
Query Match 99.4%; Score 2035; DB 11; Length 391;  
Best Local Similarity 99.7%; Pred. No. 1.7e-169;



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QY 121 SYRAGHTGIMKIVAQWVAVWILAFVNGPMLIASDWSKNSTNTKDCPEGFVTEWYILIT 180
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 SYRTQHTGVKIVTLWVAVVLAFLVNGPMLIVSEWDEGS--ECEPGFSEWYILAIT 178
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGSTTTSSASGHLHRAGVACRTSN 240
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 SFLEFVIVPILVAVFNMNIYWSLWKRRDLHLSRCQSHPGULTAVSSNCGHSFRGLSSRRSL 238
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 241 PGLKESAAHSRSESPPRRKSSILVSLRTHMNSITAFKVGSPWRSSESAALRQREYAEILL 300
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 SASTEVPAFSEHQRRKSSLMFSRTKNSNTTASKMGSPSQSDSVALHQREHYELLRA 298
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSYAFWLOWNSFNPNELY 360
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 299 RRLAKSLAILGVFAVCWAPYSLFTIVLSFFYSATGPKSVYRIAFWLOWNSFNPNELY 358
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 361 PLCHRRFQKAFWKILCVTKWPALSQ--NQSVS 391
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 359 PLCHRRFQKAFKIFCIKKQPLSQHSRSVS 390
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 4
Q8WNV9
ID Q8WNV9 PRELIMINARY; PRT; 390 AA.
AC Q8WNV9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histamine H4 receptor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RT "cDNA cloning and characterization of porcine histamine H4 receptor.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AB053300; BAB83078.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 390 AA; 44483 MW; BC8FD363A6F4D3F CRC64;

Query Match 64.0%; Score 1311.5; DB 6; Length 390;
Best Local Similarity 65.9%; Pred. No. 2.7e-106;
Matches 299; Conservative 33; Mismatches 96; Indels 5; Gaps 3;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDNRNLHRSNYFFNLIA 58
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MSAINDTNTPLNTRIALAFMLSULLVIMLGNAVILAFVVDNRNLHRSNYFFNLIA 60
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 59 ISDFVLGLISIPLYPIHVLNPNWNGSGICMFWLITDYLLCTASVYNIIVLSYDRYQSVSN 118
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 ISDFVGVISIPLYPIHTLFKWLKLEONICAFWLIIDYLLCTASVYNIIVLSYDRYQSVSN 120
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 119 AVSYRAQHTGIMKIVAQWVAVWILAFVNGPMLIASDWSKNSTNTKDCPEGFVTEWYILIT 178
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 AVSYRTQHTGILKIVALMVGVWVLAFLVHGPVILVSEAMKQ--GKQDCEFGFLKEWYVLA 178
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 179 ITMLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGSTTTSSASGHLHRAGVACRT 238
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 ITLFEFLAPVLLVAYFNLXYIYWSLWKRGHLSRCQSHCGLTPVSSGWSGHSRCPGLFGR 238
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 239 SNPGLKESAAHSRSESPPRRKSSILVSLRTHMNSITAFKVGSPWRSSESAALRQREYAEILL 298
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 SLSDPKESAAAALSHSERPPRRKSTLWFSLRTRM--SSLTASNKGFLSHSDSLALHQEHLLE 297
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 299 RGRKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSYAFWLOWNSFNPNFP 358
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 298 RARLARSAILLGVFAICWAPYSLTITRSVYPTNPFPPSTAVYKFAFWLOWNSFCVNPFF 357
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 359 LYPCLCHRRFQKAFWKILCVTKWPALSQ--NQSVS 391
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 358 LYPCLCHRRFQKAFKIFCLKKQSTLSHNRSTSS 390
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 5
Q91ZY3
ID Q91ZY3 PRELIMINARY; PRT; 389 AA.
AC Q91ZY3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histamine H4 receptor.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
RT "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor
RT suggests substantial species variation.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF358858; AAK97379.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 389 AA; 44511 MW; 51AF32FD6F1C3B4F CRC64;

Query Match 60.4%; Score 1238; DB 11; Length 389;
Best Local Similarity 62.5%; Pred. No. 7e-100;
Matches 245; Conservative 43; Mismatches 100; Indels 4; Gaps 3;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVAVILAFVVDNRNLHRSNYFFNLIA 60
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MLANST-IALTSIKISLTFLMSLLAIAIMLGNAVILAFVVDNRNLHRSNYFFNLIA 59
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 DFLVGLISIPLYPIHVLNPNWNGSGICMFWLITDYLLCTASVYNIIVLSYDRYQSVSN 120
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 DFFVGAIALPXYIPSSLTWTSGKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVSN 119
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 SYRAGHTGIMKIVAQWVAVWILAFVNGPMLIASDWSKNSTNTKDCPEGFVTEWYILIT 180
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 120 WYRAQSGTGMKIVATQWVAVVIFSMFNGPMLISDSWQNSTT--ECEPGFLKWKYFALPT 177
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGF--STTSSASGHLHRAGVACRTS 239
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 178 SLLEFLIPILLVAYFSAHIYWSLWKREKLSRCLSHVPLPSDSSSDHGHSCRPDPSRAT 237
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 240 NPLKESAAHSRSESPPRRKSSILVSLRTHMNSITAFKVGSPWRSSESAALRQREYAEILL 299
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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QY 311 LSFAICWAPYCLFTIVLSTYPTERPKSVVYSIAFWLQWNSFVNPLYPLCHRRFOKA 370
Db 284 VSIFGLCWAPYTLMIIRAACHGHCVP-DYWYETSFLLWANSVNPVLYPLCHHSFRA 342
QY 371 FWKILCVTK 379
Db 343 FTKLLCPQK 351

RESULT 8
Q8WXZ9 PRELIMINARY; PRT; 373 AA.
AC Q8WXZ9
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histamine H3 receptor isoform 4.
GN HRH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Braun M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321913; AAL71914.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR00276; GPCR Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 373 AA; 41570 MW; FAE9DFC5C3AF4DE9 CRC64;

Query Match 32.5%; Score 665.5; DB 4; Length 373;
Best Local Similarity 40.1%; Pred. No. 6.9e-50;
Matches 148; Conservative 46; Mismatches 114; Indels 61; Gaps 8;

QY 18 LAFLMSSFAFAIMGVNAVILAFVVDRLNRHRSNYFFLNLAISDFLVGLISIPLYPHVL 77
Db 37 LAALMALLIVATVGLNALVMAFVADSSLRTONNFFLLNLAISDFLVGAFCLPLYVPYL 96
QY 78 F-NNFGSGICMFWLITDYLLCTASVYNTVLISYDRYQSVNAVSYRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVDVYLLCTSSAFNLVLSYDRFLSVTRAVSYRAQQTTRAVRQM 156
QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTKDCPGVFTWYITITMLLEFLPVIS 191
Db 157 LLVWVLAFLLYGPAFL--SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSNPGLKESASRH 251
Db 214 VTFFNLISVLIQRTREL-----RLDGEAAAGPEPPPEAQPS 252
QY 252 SSSPRKKSILVSLRTHMNSSITAFKVGFWRSSEAALEQREYAEILL-RGRKLARSALIL 310
Db 253 PPPP-----GCW-----GCWQKHGGEAMPLHRVAKSLAVI 283
QY 311 LSFAICWAPYCLFTIVLSTYPTERPKSVVYSIAFWLQWNSFVNPLYPLCHRRFOKA 370
Db 284 VSIFGLCWAPYTLMIIRAACHGHCVP-DYWYETSFLLWANSVNPVLYPLCHHSFRA 342
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QY 371 FWKILCVTK 379
Db 343 FTKLLCPQK 351

RESULT 9
Q8WY00 PRELIMINARY; PRT; 301 AA.
AC Q8WY00;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histamine H3 receptor isoform 3.
GN HRH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Braun M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321912; AAL71913.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR00276; GPCR Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 301 AA; 33280 MW; EE740A2E0AB93CC9 CRC64;

Query Match 24.0%; Score 492.5; DB 4; Length 301;
Best Local Similarity 50.5%; Pred. No. 6.9e-35;
Matches 100; Conservative 30; Mismatches 59; Indels 9; Gaps 3;

QY 18 LAFLMSSFAFAIMGVNAVILAFVVDRLNRHRSNYFFLNLAISDFLVGLISIPLYPHVL 77
Db 37 LAALMALLIVATVGLNALVMAFVADSSLRTONNFFLLNLAISDFLVGAFCLPLYVPYL 96
QY 78 F-NNFGSGICMFWLITDYLLCTASVYNTVLISYDRYQSVNAVSYRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVDVYLLCTSSAFNLVLSYDRFLSVTRAVSYRAQQTTRAVRQM 156
QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTKDCPGVFTWYITITMLLEFLPVIS 191
Db 157 LLVWVLAFLLYGPAFL--SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VAYFNVQIYWSLWKRRAL 209
Db 214 VTFFNLISVLIQRTREL 231

RESULT 10
Q8NI49 PRELIMINARY; PRT; 309 AA.
AC Q8NI49;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histamine H3 receptor isoform 6.
GN HRH3.
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P., Goodman M.W., Bursstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Neuropharmacology 0:0-0(2002).
DR EMBL; AF46904; AAM43829.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:000276; GPCR_Rhodopsn.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 309 AA; 34242 MW; B7496F7D1D2A206B CRC64;

Query Match 24.0%; Score 492.5; DB 4; Length 309;
Best Local Similarity 50.5%; Pred. No. 7.1e-35;
Matches 100; Conservative 30; Mismatches 59; Indels 9; Gaps 3;

QY 18 LAFMSSFAFAIMGVNAVVLAVFVVDRLNRHSNYFFNLALISDFVLGLISIPLYIPHL 77
D 18 LAFMSSFAFAIMGVNAVVLAVFVVDRLNRHSNYFFNLALISDFVLGLISIPLYIPHL 77
DB 18 LAFMSSFAFAIMGVNAVVLAVFVVDRLNRHSNYFFNLALISDFVLGLISIPLYIPHL 77
QY 37 LAALMALLIVATVLGNALVLAADVADSSLTQNNFFLLNLALISDFVLGAFCIPLVYPVL 96
D 37 LAALMALLIVATVLGNALVLAADVADSSLTQNNFFLLNLALISDFVLGAFCIPLVYPVL 96
DB 37 LAALMALLIVATVLGNALVLAADVADSSLTQNNFFLLNLALISDFVLGAFCIPLVYPVL 96
QY 78 F-NNFSGSGICMFWLITDYLLCTASVYNIIVLISDYRQSVNAVSYRAQHTGIMKIVQM 136
D 78 F-NNFSGSGICMFWLITDYLLCTASVYNIIVLISDYRQSVNAVSYRAQHTGIMKIVQM 136
DB 78 F-NNFSGSGICMFWLITDYLLCTASVYNIIVLISDYRQSVNAVSYRAQHTGIMKIVQM 136
QY 97 TGRWTFGRGLCKLWLVVDVLLCTSSAFNLVLSYDFSVRAVSYRAQOGDTRAVRM 156
D 97 TGRWTFGRGLCKLWLVVDVLLCTSSAFNLVLSYDFSVRAVSYRAQOGDTRAVRM 156
DB 97 TGRWTFGRGLCKLWLVVDVLLCTSSAFNLVLSYDFSVRAVSYRAQOGDTRAVRM 156
QY 137 VAVVTLAFLVNGPMILASDSK-----NSTNTKDCPGFVTEWVLTITMLLEFLLPVIS 191
D 137 VAVVTLAFLVNGPMILASDSK-----NSTNTKDCPGFVTEWVLTITMLLEFLLPVIS 191
DB 137 VAVVTLAFLVNGPMILASDSK-----NSTNTKDCPGFVTEWVLTITMLLEFLLPVIS 191
QY 157 LLVWVLAFLLYGPAIL---SWEVLSSGSIPEGHGCAEFFYNNYFLITASTLEFTEPFLS 213
D 157 LLVWVLAFLLYGPAIL---SWEVLSSGSIPEGHGCAEFFYNNYFLITASTLEFTEPFLS 213
DB 157 LLVWVLAFLLYGPAIL---SWEVLSSGSIPEGHGCAEFFYNNYFLITASTLEFTEPFLS 213
QY 192 VAYFNVQIYWSLWKRRL 209
D 192 VAYFNVQIYWSLWKRRL 209
DB 192 VAYFNVQIYWSLWKRRL 209
QY 214 VTFNLSIYLNQRRRL 231
D 214 VTFNLSIYLNQRRRL 231
DB 214 VTFNLSIYLNQRRRL 231

RESULT 11
Q8VH24 PRELIMINARY; PRT; 530 AA.
AC Q8VH24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Muscarinic receptor 5.
GN GPM5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
CX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA So I., Yang D., Kim H., Min K., Kim S., Kim K., Park K., Choi K.,
RA Kim I.;
RT "Five subtypes of muscarinic receptors are expressed in gastric smooth
RT muscles of guinea pig.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC EMBL; AY072062; AAL67913.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 309 AA; 34242 MW; B7496F7D1D2A206B CRC64;

Query Match 20.3%; Score 415.5; DB 11; Length 530;
Best Local Similarity 25.9%; Pred. No. 7.2e-28;
Matches 128; Conservative 86; Mismatches 140; Indels 141; Gaps 16;

QY 16 VPLAFLMSSFAFAIMGVNAVVLAVFVVDRLNRHSNYFFNLALISDFVLGLISIPLYIPHL 75
D 16 VPLAFLMSSFAFAIMGVNAVVLAVFVVDRLNRHSNYFFNLALISDFVLGLISIPLYIPHL 75
DB 16 VPLAFLMSSFAFAIMGVNAVVLAVFVVDRLNRHSNYFFNLALISDFVLGLISIPLYIPHL 75
QY 31 VTIAAVSAVSLTIVGNVLMVIFSKNSQLTKVNNYFLSLACADLIIGVFSNNLYTY 90
D 31 VTIAAVSAVSLTIVGNVLMVIFSKNSQLTKVNNYFLSLACADLIIGVFSNNLYTY 90
DB 31 VTIAAVSAVSLTIVGNVLMVIFSKNSQLTKVNNYFLSLACADLIIGVFSNNLYTY 90
QY 76 VLF-NNFSGSGICMFWLITDYLLCTASVYNIIVLISDYRQSVNAVSYRAQHT-----GIM 130
D 76 VLF-NNFSGSGICMFWLITDYLLCTASVYNIIVLISDYRQSVNAVSYRAQHT-----GIM 130
DB 76 VLF-NNFSGSGICMFWLITDYLLCTASVYNIIVLISDYRQSVNAVSYRAQHT-----GIM 130
QY 91 ILMGWALGSLACDLWLDLVASNASVMNLLVISDFRYFSITRPLTYRAKRTPKRAGIL 150
D 91 ILMGWALGSLACDLWLDLVASNASVMNLLVISDFRYFSITRPLTYRAKRTPKRAGIL 150
DB 91 ILMGWALGSLACDLWLDLVASNASVMNLLVISDFRYFSITRPLTYRAKRTPKRAGIL 150
QY 131 KIVAQVAVWILAFVNGPMILASDSW-----KNSNTKDCPGFVTEWVLTITMLLEF 185
D 131 KIVAQVAVWILAFVNGPMILASDSW-----KNSNTKDCPGFVTEWVLTITMLLEF 185
DB 131 KIVAQVAVWILAFVNGPMILASDSW-----KNSNTKDCPGFVTEWVLTITMLLEF 185
QY 151 IGLA-----WLVSFILWAPAILC---WQYLVGKRTVPPDECQIQFLSEPTITFTGTAIAAF 202
D 151 IGLA-----WLVSFILWAPAILC---WQYLVGKRTVPPDECQIQFLSEPTITFTGTAIAAF 202
DB 151 IGLA-----WLVSFILWAPAILC---WQYLVGKRTVPPDECQIQFLSEPTITFTGTAIAAF 202
QY 186 LLPVISVAYFNVQIYWSLWKR-----RALSR-----CP----- 213
D 186 LLPVISVAYFNVQIYWSLWKR-----RALSR-----CP----- 213
DB 186 LLPVISVAYFNVQIYWSLWKR-----RALSR-----CP----- 213
QY 203 YVPSVMTILYCRYIRETEKTKDLAELOGSDSVAAAKRRPAPRALRSCFSPHPTLV 262
D 203 YVPSVMTILYCRYIRETEKTKDLAELOGSDSVAAAKRRPAPRALRSCFSPHPTLV 262
DB 203 YVPSVMTILYCRYIRETEKTKDLAELOGSDSVAAAKRRPAPRALRSCFSPHPTLV 262
QY 214 ----SHAGFST-----TSSASGH-LHRAVY-----ACRTSNPGIK 244
D 214 ----SHAGFST-----TSSASGH-LHRAVY-----ACRTSNPGIK 244
DB 214 ----SHAGFST-----TSSASGH-LHRAVY-----ACRTSNPGIK 244
QY 263 QRERSQASWSSSRKSTSTSGTPSQATGSHAHWKVGQLATSRYPVPEDEAQPADPVFQ 322
D 263 QRERSQASWSSSRKSTSTSGTPSQATGSHAHWKVGQLATSRYPVPEDEAQPADPVFQ 322
DB 263 QRERSQASWSSSRKSTSTSGTPSQATGSHAHWKVGQLATSRYPVPEDEAQPADPVFQ 322
QY 245 ESAASRHSESPRRKSSILVLRTHMS---SITAFKVSFWSESAAALR----- 290
D 245 ESAASRHSESPRRKSSILVLRTHMS---SITAFKVSFWSESAAALR----- 290
DB 245 ESAASRHSESPRRKSSILVLRTHMS---SITAFKVSFWSESAAALR----- 290
QY 323 AVYNSQAKESPRESLSAKEAKEKAVKQREKTDYDIPKIFLSPAAAHRLKSKQCVAYKFK 382
D 323 AVYNSQAKESPRESLSAKEAKEKAVKQREKTDYDIPKIFLSPAAAHRLKSKQCVAYKFK 382
DB 323 AVYNSQAKESPRESLSAKEAKEKAVKQREKTDYDIPKIFLSPAAAHRLKSKQCVAYKFK 382
QY 291 -----QREYAEILLRGRKLAR 305
D 291 -----QREYAEILLRGRKLAR 305
DB 291 -----QREYAEILLRGRKLAR 305
QY 383 LVVKADGQETNGCRKVKIMPCFPVSKGTPSKGLEPNLSHQMTKRRKRWLVKERRKAAQ 442
D 383 LVVKADGQETNGCRKVKIMPCFPVSKGTPSKGLEPNLSHQMTKRRKRWLVKERRKAAQ 442
DB 383 LVVKADGQETNGCRKVKIMPCFPVSKGTPSKGLEPNLSHQMTKRRKRWLVKERRKAAQ 442
QY 306 SLAILLSAFICWAPCYCLFTIVLSTYPTERPKSVVYIAFWLQWNFNFVNPFLPLCHR 365
D 306 SLAILLSAFICWAPCYCLFTIVLSTYPTERPKSVVYIAFWLQWNFNFVNPFLPLCHR 365
DB 306 SLAILLSAFICWAPCYCLFTIVLSTYPTERPKSVVYIAFWLQWNFNFVNPFLPLCHR 365
QY 443 TLSAILLAFILWTPTYNIMLV-STFCDTCIPVLWH-LGYWLCYVNSTVNPICVALCNR 500
D 443 TLSAILLAFILWTPTYNIMLV-STFCDTCIPVLWH-LGYWLCYVNSTVNPICVALCNR 500
DB 443 TLSAILLAFILWTPTYNIMLV-STFCDTCIPVLWH-LGYWLCYVNSTVNPICVALCNR 500
QY 366 RPKAFWKILCVTKW 380
D 366 RPKAFWKILCVTKW 380
DB 366 RPKAFWKILCVTKW 380
QY 501 TFRKTF-KMLLLCRW 514
D 501 TFRKTF-KMLLLCRW 514
DB 501 TFRKTF-KMLLLCRW 514

RESULT 12
Q96RH1 PRELIMINARY; PRT; 454 AA.
AC Q96RH1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE M1 muscarinic cholinergic receptor.
GN CHRM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J., Grando S.A.;
RT "Cloning Cholinergic Receptors in Human Keratinocytes.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC EMBL; AF385587; AAK68112.1; -.
DR
```

[illegible]

Search completed: October 1, 2004, 10:12:40  
Job time : 48 secs



GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: October 1, 2004, 10:13:10 ; Search time 125 Seconds  
(without alignments)  
803.809 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 391

Sequence: 1 MSNSTGILPPAAQVPLAF.....WKILCVTKWPAISQNSVSS 391

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : 1: A Geneseq\_29Jan04.\*

2: Geneseqp1980s.\*

3: Geneseqp1990s.\*

4: Geneseqp2000s.\*

5: Geneseqp2001s.\*

6: Geneseqp2002s.\*

7: Geneseqp2003as.\*

8: Geneseqp2003bs.\*

9: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	379	96.9	391	5	AAM50565
2	33	8.4	391	5	AAM50566
3	32	8.2	389	5	AAM50567
4	21	5.4	73	4	AAG80931
5	21	5.4	73	5	ABG93749
6	21	5.4	357	6	ABG93749 Human G p
7	21	5.4	390	3	AAB02831
8	21	5.4	390	3	AAY71297
9	21	5.4	390	4	AAB62445
10	21	5.4	390	4	AAG64477
11	21	5.4	390	4	AAM51410
12	21	5.4	390	4	AAB73622
13	21	5.4	390	5	AAM53050
14	21	5.4	390	5	ABP98629
15	21	5.4	390	5	ABP98629 Human his
16	21	5.4	390	5	Abb78276 Amino aci
17	21	5.4	390	5	AAM50564
18	21	5.4	390	5	AAG66023
19	21	5.4	390	5	AAU74906
20	21	5.4	390	6	ABG71960
21	21	5.4	390	6	ABU92265
22	21	5.4	390	6	ABP81727
23	21	5.4	390	6	AAE36417
24	21	5.4	390	6	AAE36416
25	21	5.4	391	5	AAM53052
			392	5	AAM53053

#### ALIGNMENTS

##### RESULT 1

AAM50565

ID AAM50565 standard; protein; 391 AA.

XX AC

XX AAM50565;

XX AC

DT 18-MAR-2002 (first entry)

XX AC

DE Mouse histamine H4 receptor.

XX AC

KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy.

XX AC

OS Mus musculus.

XX AC

PN WO200192485-A1.

XX AC

PD 06-DEC-2001.

XX AC

PF 22-FEB-2001; 2001WO-US005914.

XX AC

PR 31-MAY-2000; 2000US-0208260P.

XX AC

PA (ORTH ) ORTHO-MCNEIL PHARM INC.

XX AC

PI Lovenberg T, Liu C;

XX AC

DR WPI; 2002-114339/15.

XX AC

N-PSDB; AAI70981.

XX AC

PS New mammalian histamine H4 receptor proteins and polynucleotides encoding

XX AC

CC the proteins, useful in gene therapy for treating diseases where it is

CC beneficial to elevate mammalian histamine H4 receptor activity.

XX AC

Claim 13; Fig 5B; 92pp; English.

XX AC

CC The present sequence is that of a mouse histamine receptor of the H4

CC subtype, as predicted from a cDNA clone isolated from a spleen cDNA

CC library. The invention provides mammalian (human, mouse, rat and guinea

CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and

CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in

CC recombinant host cells that produce active recombinant protein. The

CC pharmacology of known histamine ligands is demonstrated. Mammalian

CC histamine H4 receptor may be used in gene therapy for the treatment of

CC diseases where it is beneficial to elevate mammalian histamine H4

CC receptor activity. Recombinant protein is useful for identifying

CC modulators of the histamine H4 receptor. Such modulators may be useful

Aae23411 Human G-p  
Abg28404 Novel hum  
Abg25785 Novel hum  
Aae36414 Human H4  
Aaw92979 Human mAC  
Aag67833 Human mAC  
Aag67840 Rat mACHR  
Abg76408 Human mus  
Abg76415 Rat musca  
Aau25653 G protein  
Aau27516 Human G-P  
Aao29538 Human H3  
Aao29537 Human H3  
Aao29532 Human H3  
Aao29531 Human H3  
Aao29535 Human H3  
Aab82911 Human his  
Aag65581 Human his  
Aag65580 Human his  
Aao29528 Human H3

26 21 5.4 441 5 AAE23411  
27 21 5.4 592 4 ABG28404  
28 21 5.4 592 4 ABG25785  
29 14 3.6 336 6 AAE36414  
30 11 2.8 19 2 AAW92979  
31 11 2.8 19 2 AAG67833  
32 11 2.8 19 2 AAG67833  
33 11 2.8 19 2 AAG67840  
34 11 2.8 19 6 ABG76408  
35 11 2.8 19 6 ABG76415  
36 11 2.8 168 4 AAU25653  
37 11 2.8 230 4 AAU27516  
38 11 2.8 290 7 AAO29538  
39 11 2.8 293 7 AAO29537  
40 11 2.8 326 7 AAO29532  
41 11 2.8 329 7 AAO29531  
42 11 2.8 329 7 AAO29535  
43 11 2.8 340 4 AAB82911  
44 11 2.8 351 4 AAG65581  
45 11 2.8 365 4 AAG65580  
46 11 2.8 365 7 AAO29528

CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
CC the neuroendocrine system, stress and spasticity  
XX  
SQ Sequence 391 AA;  
Query Match 96.9%; Score 379; DB 5; Length 391;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSENSTGILPPAAQVPLAFMSSFAFALMVGNAVWILAFVVDNLRHRSNYFFLNLAIS 60  
Db 1 MSENSTGILPPAAQVPLAFMSSFAFALMVGNAVWILAFVVDNLRHRSNYFFLNLAIS 60  
Qy 61 DFLVGLISIPILYIPHLVFNMFNGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNV 120  
Db 61 DFLVGLISIPILYIPHLVFNMFNGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNV 120  
Qy 121 SYRAQHTGIMKIVQAVWVILAFVNGPMLASDSWKNSTNTKDCPEGFVTEWILTIT 180  
Db 121 SYRAQHTGIMKIVQAVWVILAFVNGPMLASDSWKNSTNTKDCPEGFVTEWILTIT 180  
Qy 181 MLLBFLPVIISVAVFNVQIYWSLWKRRALSRCPSHAGFTSSSSASGHLHRAGVACRTSN 240  
Db 181 MLLBFLPVIISVAVFNVQIYWSLWKRRALSRCPSHAGFTSSSSASGHLHRAGVACRTSN 240  
Qy 241 PGLKESAAASRHSSEPRKSSILVSLRTHMNSSITAFKVGSEFWRSSAALRQREYAEALLRG 300  
Db 241 PGLKESAAASRHSSEPRKSSILVSLRTHMNSSITAFKVGSEFWRSSAALRQREYAEALLRG 300  
Qy 301 RKLARSLAILLSAFALCWAPYCLFTIVLSTYPTERTPKSWYSIAPFLQWNSFVNPFILY 360  
Db 301 RKLARSLAILLSAFALCWAPYCLFTIVLSTYPTERTPKSWYSIAPFLQWNSFVNPFILY 360  
Qy 361 PLCHRRFOKAFWKILCVTK 379  
Db 361 PLCHRRFOKAFWKILCVTK 379

RESULT 2  
AAM50566  
ID AAM50566 standard; protein; 391 AA.  
XX  
AC AAM50566;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Rat histamine H4 receptor.  
XX  
KW Histamine H4 receptor; rat; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy.  
XX  
OS Rattus rattus.  
XX  
PN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Lovenberg T, Liu C;  
XX  
XX WPI; 2002-114339/15.  
DR N-PSDB; AAI70982.  
XX  
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
PT the proteins, useful in gene therapy for treating diseases where it is

PT beneficial to elevate mammalian histamine H4 receptor activity.  
XX Claim 13; Fig 6A; 92pp; English.  
XX  
CC The present sequence is that of a rat histamine receptor of the H4  
CC subtype, as predicted from a cDNA clone isolated from a spleen cDNA  
CC library. The invention provides mammalian (human, mouse, rat and guinea  
CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
CC recombinant host cells that produce active recombinant protein. The  
CC pharmacology of known histamine ligands is demonstrated. Mammalian  
CC histamine H4 receptor may be used in gene therapy for the treatment of  
CC diseases where it is beneficial to elevate mammalian histamine H4  
CC receptor activity. Recombinant protein is useful for identifying  
CC modulators of the histamine H4 receptor. Such modulators may be useful  
CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
CC the neuroendocrine system, stress and spasticity  
XX  
SQ Sequence 391 AA;  
Query Match 8.4%; Score 33; DB 5; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1 5e-24;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 131 KIVAQWAVWILAFVNGPMLASDSWKNSTNT 163  
Db 131 KIVAQWAVWILAFVNGPMLASDSWKNSTNT 163  
RESULT 3  
AAM50567  
ID AAM50567 standard; protein; 389 AA.  
XX  
AC AAM50567;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Guinea pig histamine H4 receptor.  
XX  
KW Histamine H4 receptor; guinea pig; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy.  
XX  
OS Cavia porcellus.  
XX  
PN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Lovenberg T, Liu C;  
XX  
XX WPI; 2002-114339/15.  
DR N-PSDB; AAI70983.  
XX  
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
PT the proteins, useful in gene therapy for treating diseases where it is  
XX beneficial to elevate mammalian histamine H4 receptor activity.  
XX Claim 13; Fig 6C; 92pp; English.  
XX  
CC The present sequence is that of a guinea pig histamine receptor of the H4  
CC subtype, as predicted from a cDNA clone isolated from a bone marrow  
CC library. The invention provides mammalian (human, mouse, rat and guinea  
CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in

CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the histamine H4 receptor. Such modulators may be useful  
 CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
 CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
 CC the neuroendocrine system, stress and spasticity  
 XX Sequence 389 AA;

Query Match 8.2%; Score 32; DB 5; Length 389;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-23;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 FWLITDYLCTASVYNIVLISYDRYQVSNAV 120  
 |||||  
 Db 88 FWLITDYLCTASVYNIVLISYDRYQVSNAV 119

RESULT 4  
 AAG80931  
 ID AAG80931 standard; protein; 73 AA.

AC AAG80931;

XX 28-AUG-2001 (first entry)

XX Human ngPCR4.

XX G protein-coupled receptor; ngPCR; seven transmembrane receptor;  
 KW signal transduction; schizophrenia; thyroid disorder; renal failure;  
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;  
 KW cardiovascular disease; proliferative disorder; hormonal disorder;  
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;  
 KW attention deficit-hyperactivity disorder/attention deficit disorder;  
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;  
 KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;  
 KW neuroprotective.

XX Homo sapiens.

XX WO200136473-A2.

XX 25-MAY-2001.

XX 16-NOV-2000; 2000WO-US031581.

XX 16-NOV-1999; 99US-0165838P.

XX 17-NOV-1999; 99US-0166071P.

XX 19-NOV-1999; 99US-0166678P.

XX 28-DEC-1999; 99US-0173396P.

XX 22-FEB-2000; 2000US-0184129P.

XX 28-FEB-2000; 2000US-0185421P.

XX 28-FEB-2000; 2000US-0185554P.

XX 02-MAR-2000; 2000US-0186530P.

XX 09-MAR-2000; 2000US-0186811P.

XX 17-MAR-2000; 2000US-0190310P.

XX 21-MAR-2000; 2000US-0190800P.

XX 20-APR-2000; 2000US-0198568P.

XX 02-MAY-2000; 2000US-0201190P.

XX 08-MAY-2000; 2000US-0203111P.

XX 25-MAY-2000; 2000US-0207094P.

XX (PHAA ) PHARMACIA & UPJOHN CO.

XX Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;  
 PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;  
 XX WPI; 2001-389826/41.

DR N-PSDB; AAH50971.

XX New G protein-coupled receptor (ngPCR-x) and its encoding polynucleotide  
 PT useful for diagnosing and treating e.g. schizophrenia.

XX Claim 37; Page 77; 261pp; English.

XX The present invention relates to novel G protein-coupled receptors  
 CC (ngPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,  
 CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is  
 CC one such G protein-coupled receptor. GPCRs are also known as seven  
 CC transmembrane receptors and function in signal transduction. The ngPCRx  
 CC coding sequences are useful for screening a human to diagnose a disorder  
 CC affecting the brain or a genetic predisposition, specifically  
 CC schizophrenia. ngPCRx are useful for identifying compounds useful for  
 CC treating schizophrenia. Detection of ngPCRx in a sample is useful as a  
 CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal  
 CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,  
 CC metabolic and cardiovascular diseases, proliferative disorders and  
 CC hormonal disorders. Modulators of ngPCRx activity have the utility for  
 CC treating neurological disorders, including schizophrenia, ADHD/ADD  
 CC (attention deficit-hyperactivity disorder/attention deficit disorder),  
 CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,  
 CC migraine and senile dementia. Additional disorders include inflammatory  
 CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune  
 CC disorders, cancers, respiratory ailments such as asthma, and inflammatory  
 CC diseases e.g. inflammatory bowel disease

XX Sequence 73 AA;

Query Match 5.4%; Score 21; DB 4; Length 73;

Best Local Similarity 100.0%; Pred. No. 5.1e-13;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLISYDRY 113

|||||

Db 31 TDYLLCTASVYNIVLISYDRY 51

RESULT 5

ABG93749

ID ABG93749 standard; protein; 73 AA.

XX AC ABG93749;

XX 26-NOV-2002 (first entry)

XX Human G protein-coupled receptor protein, beGPCR-seq4.

XX Human; receptor; G protein-coupled receptor; GPCR; ngPCR; beGPCR;  
 KW ng protein coupled receptor; communication; serpentine structure;  
 KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;  
 KW genetic predisposition; brain; immune response; gene therapy;  
 KW anxiety disorder; depression; bipolar disorder; schizophrenia;  
 KW Huntington's disease; dyskinesia; manic depression; stroke;  
 KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;  
 KW tranquiliser.

XX Homo sapiens.

XX WO200264789-A1.

XX 22-AUG-2002.

XX 14-FEB-2001; 2001WO-US004641.

XX 14-FEB-2001; 2001WO-US004641.

XX (PHAA ) PHARMACIA & UPJOHN CO.

XX Lind P, Parodi LA, Vogeli G, Wood LS;

XX WPI; 2002-674879/72.

```
DR N-PSDB; ABS70204.
XX
XX New nucleic acids and polypeptides of the ng protein-coupled receptor,
PT useful for treating or diagnosing a mental disorder or a disorder
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
PT Parkinson's disease.
XX
XX Example 1; Page 72; 244pp; English.
XX
XX The invention discloses an isolated human polypeptide, and encoding
XX nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
XX ng protein coupled receptor-14 (ngPCR-14). GPCRs are vital in the
XX communication between cells and their environment and are characterised
XX by a serpentine structure that passes through the cell membrane seven
XX times, hence the reason such receptors are sometimes called seven
XX transmembrane receptors (7TM). The polynucleotides and polypeptides are
XX useful for identifying an ngPCR allelic variant that correlates with a
XX mental disorder, for isolating an antibody that binds to an epitope of
XX the polypeptide, for identifying a compound that binds the polypeptide or
XX polynucleotide and/or modulates its biological activity, for screening a
XX human subject to diagnose a disorder, or a genetic predisposition to a
XX disorder, affecting the brain or a genetic disposition to the disorder,
XX for identifying compounds useful for the treatment of a mental disorder
XX and for identifying a compound useful as a modulator of binding between
XX ngPCR-14 and a binding partner of ngPCR-14. The polypeptide is also
XX useful for inducing an immune response in a mammal. The nucleic acid or
XX polypeptide is particularly useful, using gene therapy, for treating e.g.
XX anxiety disorders, depression, bipolar disorder, schizophrenia,
XX Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
XX disease or Alzheimer's disease. The nucleic acid and polypeptide may also
XX be used for treating diabetes, inflammation or wounds. The sequences
XX presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the ngPCR (also
XX referred to as beGPCRs) proteins
XX
XX Sequence 73 AA;
XX
XX Query Match 5.4%; Score 21; DB 5; Length 73;
XX Best Local Similarity 100.0%; Pred. No. 5.1e-13;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 93 TDYLLCTASVNVNVLISYDRY 113
XX |||||
XX Db 31 TDYLLCTASVNVNVLISYDRY 51
XX
XX RESULT 6
XX AAE36415
XX ID AAE36415 standard; protein; 357 AA.
XX AC AAE36415;
XX XX
XX DT 07-AUG-2003 (first entry)
XX XX
XX DE Human H4 receptor splice variant (H4c) protein.
XX
XX XX
XX KW Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;
XX atopic dermatitis; stroke; myocardial infarction; migraine; allergy;
XX chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;
XX rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;
XX asthma; receptor; variant.
XX
XX OS Homo sapiens.
XX
XX XX
XX PN WO2003020907-A2.
XX
XX PD 13-MAR-2003.
XX
XX XX
XX PF 30-AUG-2002; 2002WO-US027891.
XX
XX XX
XX PR 31-AUG-2001; 2001US-0316762P.
XX
XX PR 13-NOV-2001; 2001US-0332697P.
XX
XX XX
XX PA (MERI ) MERCK & CO INC.
XX
XX Gallagher MJ, Yates SL;
XX
XX WPI; 2003-290186/28.
XX
XX N-PSDB; AAD55124.
XX
XX Novel splice variants of human H4 histamine receptor, H4b and H4c, useful
XX for identifying agonists or antagonists of the receptor which are useful
XX for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
XX
XX Claim 21; Page 50-51; 3lpp; English.
XX
XX The invention relates to splice variants of human H4 histamine receptor,
XX H4b and H4c. The invention is useful for identifying an agonist,
XX antagonist or inverse agonist of a mammalian histamine receptor. The
XX agonist, antagonist or inverse agonist of H4b and H4c is useful for
XX treating inflammation, asthma, allergy, atopic dermatitis, stroke,
XX myocardial infarction, migraine, chronic obstructive pulmonary disease
XX (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel
XX disease, or psoriasis. The present sequence is human H4c protein
XX
XX Sequence 357 AA;
XX
XX Query Match 5.4%; Score 21; DB 6; Length 357;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-12;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 93 TDYLLCTASVNVNVLISYDRY 113
XX |||||
XX Db 93 TDYLLCTASVNVNVLISYDRY 113
XX
XX RESULT 7
XX AAB02831
XX ID AAB02831 standard; protein; 390 AA.
XX AC AAB02831;
XX XX
XX DT 22-AUG-2000 (first entry)
XX XX
XX DE Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.
XX
XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX identification; agonist; screening; therapeutic; pharmaceutical; mutant.
XX
XX OS Homo sapiens.
XX
XX XX
XX PN WO200022131-A2.
XX
XX PD 20-APR-2000.
XX
XX PF 13-OCT-1999; 99WO-US024065.
XX
XX PR 13-OCT-1998; 98US-00170496.
XX
XX PR 12-NOV-1998; 98US-0108029P.
XX
XX PR 20-NOV-1998; 98US-0109213P.
XX
XX PR 27-NOV-1998; 98US-0110060P.
XX
XX PR 16-FEB-1999; 99US-0120416P.
XX
XX PR 26-FEB-1999; 99US-0121852P.
XX
XX PR 12-MAR-1999; 99US-0123944P.
XX
XX PR 12-MAR-1999; 99US-0123945P.
XX
XX PR 12-MAR-1999; 99US-0123946P.
XX
XX PR 12-MAR-1999; 99US-0123948P.
XX
XX PR 12-MAR-1999; 99US-0123949P.
XX
XX PR 12-MAR-1999; 99US-0123951P.
XX
XX PR 28-MAY-1999; 99US-0136436P.
XX
XX PR 28-MAY-1999; 99US-0136437P.
XX
XX PR 28-MAY-1999; 99US-0136439P.
XX
XX PR 28-MAY-1999; 99US-0137127P.
XX
XX PR 28-MAY-1999; 99US-0137131P.
XX
XX PR 28-MAY-1999; 99US-0137567P.
XX
XX PR 29-JUN-1999; 99US-0141448P.
XX
XX PR 27-AUG-1999; 99US-0151114P.
```

PR 03-SEP-1999; 99US-0152524P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156633P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 29-SEP-1999; 99US-0156653P.  
 PR 01-OCT-1999; 99US-0157280P.  
 PR 01-OCT-1999; 99US-0157281P.  
 PR 01-OCT-1999; 99US-0157282P.  
 PR 01-OCT-1999; 99US-0157293P.  
 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 PR 12-OCT-1999; 99US-00417044.  
 XX (AREN-) ARENA PHARM INC.  
 XX  
 PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;  
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;  
 XX  
 DR WPI; 2000-317986/27.  
 DR N-PSDB; AAA46023.  
 XX  
 PT Non-endogenous, human G protein-coupled receptors for screening receptor,  
 PT inverse or partial agonists useful as therapeutic agents.  
 XX  
 PS Example 1; Page 89-90; 187pp; English.  
 XX  
 CC The present invention describes transmembrane receptors, preferably human  
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is  
 CC unknown (orphan GPCR receptors). More specifically the present invention  
 CC relates to non-endogenous, constitutively activated versions of a human  
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct  
 CC identification of candidate compounds as receptors agonists, inverse  
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017  
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 390 AA;  
 Query Match 5.4%; Score 21; DB 3; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 93 TDYLLCTASVYNIVLISYDRY 113  
 Db 93 TDYLLCTASVYNIVLISYDRY 113  
 XX  
 RESULT 8  
 AAY71297  
 ID AAY71297 standard; protein; 390 AA.  
 XX  
 AC AAY71297;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Human orphan G protein-coupled receptor hrUP7.  
 XX  
 KW Human; orphan G protein-coupled receptor; GPCR; hrUP7; drug screening;  
 KW transmembrane receptor; signal cascade.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200031258-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 13-OCT-1999; 99WO-US023687.  
 XX  
 PR 20-NOV-1998; 98WO-0109213P.  
 PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123949P.

PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.  
 PR 28-MAY-1999; 99US-0136567P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 29-JUN-1999; 99US-0141448P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156633P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 01-OCT-1999; 99US-0156653P.  
 PR 01-OCT-1999; 99US-0157280P.  
 PR 01-OCT-1999; 99US-0157281P.  
 PR 01-OCT-1999; 99US-0157282P.  
 PR 01-OCT-1999; 99US-0157293P.  
 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 PR 12-OCT-1999; 99US-00417044.  
 XX (AREN-) ARENA PHARM INC.  
 XX  
 PI Chen R, Dang HT, Liaw CW, Lin I;  
 XX  
 DR WPI; 2000-400068/34.  
 DR N-PSDB; AAD01124.  
 XX  
 PT Novel human orphan G protein-coupled receptors and the encoding cDNAs for  
 PT use in the identification of G protein-coupled receptor agonists.  
 XX  
 PS Claim 26; Page 60-61; 102pp; English.  
 XX  
 CC The present amino acid sequence is the hrUP7, an endogenous human orphan  
 CC G protein-coupled receptor (GPCR). The full length hrUP7 cDNA was cloned  
 CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan  
 CC GPCR of the invention, like all GPCRs has seven transmembrane alpha  
 CC helices with an extracellular N-terminus and an intracellular C-terminus.  
 CC However, no endogenous ligands has yet been identified for the proteins  
 CC of the invention. The orphan GPCRs may be used in the identification of  
 CC their endogenous ligands, and to screen potential GPCR agonists and  
 CC antagonists for use as pharmaceutical agents. The proteins may also be  
 CC used in the study of GPCR-mediated signalling cascades, and to elucidate  
 CC their precise role in normal and diseased human conditions, and to elucidate  
 CC encoding human orphan GPCRs may be used for tissue localisation  
 CC expression analysis to provide information about their function in  
 CC healthy and pathological states  
 XX  
 SQ Sequence 390 AA;  
 Query Match 5.4%; Score 21; DB 3; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 93 TDYLLCTASVYNIVLISYDRY 113  
 Db 93 TDYLLCTASVYNIVLISYDRY 113  
 XX  
 RESULT 9  
 AAB62445  
 ID AAB62445 standard; protein; 390 AA.  
 XX  
 AC AAB62445;  
 XX  
 DT 09-JUL-2001 (first entry)  
 XX  
 DE Human GPCR-like polypeptide, PFI-013.  
 XX  
 KW G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;  
 KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;  
 KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;  
 KW signal transduction.  
 XX  
 OS Homo sapiens.

```

XX PN EF1096009-A1.
XX PD
XX PF
XX PD 02-MAY-2001.
XX PF
XX PD 24-OCT-2000; 2000EP-00309364.
XX PR
XX PR 29-OCT-1999; 99GB-00025641.
XX PR 20-APR-2000; 2000GB-00009973.
XX PA (PFI) PFIZER LTD.
XX PA (PFI) PFIZER INC.
XX PI Peter B, O'reilly MA;
XX PD WPI; 2001-309854/33.
XX DR N-PSDB; AAF83203.
XX PD
XX PD New G-protein coupled receptor-like polypeptide, polynucleotide for
XX PD screening drug candidates for treating diseases associated with signal
XX PD transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
XX PS
XX PS Claim 22; Page 44; 66pp; English.
XX PD
XX PD This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-
XX PD 013, encoded by cDNA of NCIMB 41073. The PFI-013 protein can be expressed
XX PD by standard recombinant methodology. Antibodies and modulators of PFI-013
XX PD are useful in the manufacture of a medicament for treating allergic
XX PD disorder, including extrinsic asthma, immunological disorders, such as
XX PD intrinsic asthma, vasculitic granulomatous disease, interstitial and
XX PD other pulmonary disease, including chronic obstructive pulmonary disease
XX PD (COPD), infectious, inflammatory disease, such as inflammatory bowel
XX PD disease and neoplastic and myeloproliferative diseases. They are also
XX PD useful for treating obesity, diabetes, reproduction and sexual medicine,
XX PD psychotherapeutics, urogenital disease, dermatology, photoaging, skin
XX PD inflammation, cancer, tissue repair, cardiovascular, gastrointestinal diseases,
XX PD pigmentation, osteoporosis, cardiovascular, sensory organ disorders, sleep disorders
XX PD allergy and respiratory disease, sensory organ disorders, sleep disorders
XX PD and hair loss. The PFI-013 protein and nucleic acid are useful in the
XX PD diagnosis and treatment of the above conditions and also for screening
XX PD drug candidates for the treatment of diseases associated with signal
XX PD transduction. The antibodies are also useful for enrichment of
XX PD eosinophils from mammalian, especially human blood and for detecting the
XX PD protein in biological samples
XX PD
XX PD Sequence 390 AA;
XX PD
XX PD Query Match 5.4%; Score 21; DB 4; Length 390;
XX PD Best Local Similarity 100.0%; Pred. No. 2.6e-12;
XX PD Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX PD
XX PD QY 93 TDYLLCTASVYNIVLISYDRY 113
XX PD |||||
XX PD Db 93 TDYLLCTASVYNIVLISYDRY 113
XX PD
XX PD RESULT 11
XX PD AAM51410
XX PD ID AAM51410 standard; protein; 390 AA.
XX PD AC AAM51410;
XX PD XX
XX PD DT 07-JAN-2002 (first entry)
XX PD
XX PD DE Human GPRV53.
XX PD XX
XX PD KW Human; guanosine triphosphate-binding protein-coupled receptor; GPRV53;
XX PD intracellular calcium ion regulation; histamine receptor; leukocyte.
XX PD XX
XX PD OS Homo sapiens.
XX PD XX
XX PD PN WO200173023-A1.
XX PD PD
XX PD PD 04-OCT-2001.
XX PD XX
XX PD PF 30-MAR-2001; 2001WO-JP002767.
XX PD XX
XX PD PR 31-MAR-2000; 2000JP-00101339.
XX PD PR 29-MAY-2000; 2000JP-00163147.
XX PD PR 19-JUL-2000; 2000JP-00223870.
XX PD XX
XX PD PA (HELI-) HELIX RES INST.
XX PD XX
XX PD PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
XX PD PI Sugiyama T;
XX PD XX
XX PD DR WPI; 2001-626265/72.
XX PD DR N-PSDB; AAI66009.
XX PD XX

```

PT Gene encoding a G-protein coupled histamine receptor protein for  
 PT identification of agonists and antagonists as drugs active in histamine-  
 PT related disorders.

XX Claim 1; Page 42-43; 5lpp; Japanese.

XX The invention relates to human G-protein coupled histamine receptor  
 CC GPRV53. GPRV53 is a new type of histamine receptor which is  
 CC preferentially expressed in peripheral leukocytes and on stimulation with  
 CC histamine causes a change in intracellular calcium ion concentration.  
 CC GPRV53 is useful in the identification of antagonists and agonists of  
 CC histamine binding to GPRV53 which can be used for the treatment and  
 CC prevention of histamine-associated disorders. Also, since the receptor  
 CC protein is preferentially expressed in tissues (especially in peripheral  
 CC leukocytes) other than those associated with the known histamine receptor  
 CC types H1-H3 it is useful in the investigation of the role of histamine  
 CC and its receptors in the tissues in which it is expressed

XX Sequence 390 AA;

Query Match 5.4%; Score 21; DB 4; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLISYDRY 113  
 |||||  
 Db 93 TDYLLCTASVYNIVLISYDRY 113

RESULT 12

ID AAB73622

AC AAB73622 standard; protein; 390 AA.

XX AAB73622;

DT 10-AUG-2001 (first entry)

DE Human G protein-coupled receptor AXOR35.

XX AXOR35; human; G protein-coupled receptor; 7TM receptor;  
 KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;  
 KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;  
 KW bulimia; osteoporosis; asthma; allergy; urinary retention;  
 KW acute heart failure; hypotension; hypertension; angina pectoris;  
 KW myocardial infarction; stroke; ulcer; migraine; vomiting;  
 KW psychotic disorder; neurological disorder; anxiety; schizophrenia;  
 KW manic depression; bipolar disorder; depression; delirium; dementia;  
 KW severe mental retardation; dyskinesia; Parkinson's disease;  
 KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;  
 KW macrophage; eosinophil; neutrophil; function modulation;  
 KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;  
 KW drug screening; signal transduction; transgenic animal; drug discovery.

XX Homo sapiens.

XX WO200133221-A1.

XX 10-MAY-2001.

XX 26-OCT-2000; 2000WO-US029461.

XX 02-NOV-1999; 99US-00431898.

XX 03-FEB-2000; 2000US-00497790.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Aubart KM, Bergema DJ, Fitzgerald LR, Graybill TL, Li X;

XX Michalovich D, Morrow DM, Zhu Y;

XX WPI: 2001-316464/33.

XX N-PSDB; AAB24007.

PT Novel G-protein coupled receptor polypeptide and polynucleotide for  
 PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological  
 PT disorders and for identifying modulators useful for treating asthma.

XX Claim 1; Page 50-51; 54pp; English.

XX The invention relates to the human G protein-coupled receptor AXOR35  
 CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments  
 CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative  
 CC transmembrane domains and is involved in signal transduction. AXOR35 has  
 CC homology and structural similarity with G protein-coupled receptors such  
 CC as the human histamine H3 receptor. The invention also relates to  
 CC expression vectors and host cells comprising AXOR35 DNA, to recombinant  
 CC and nucleotides may be used to treat a wide variety of disorders  
 CC including bacterial, fungal, protozoal and viral infections, particularly  
 CC HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;  
 CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;  
 CC urinary retention; acute heart failure; hypotension; hypertension; angina  
 CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;  
 CC psychotic and neurological disorders such as anxiety, schizophrenia,  
 CC manic depression, depression, delirium, dementia, and severe mental  
 CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's  
 CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and  
 CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and  
 CC antibodies may be used in screening compounds for their ability to  
 CC modulate AXOR35 activity or expression. Such AXOR35 modulators are  
 CC particularly useful for treating asthma, and inhibiting or promoting the  
 CC function of lymphocytes, macrophages, eosinophils or neutrophils in  
 CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also  
 CC useful for diagnosing or determining susceptibility of an individual to a  
 CC disease via the detection of abnormal levels of protein or mRNA, or via  
 CC the detection of mutations in the corresponding gene. AXOR35 proteins are  
 CC also useful for inducing an immunological response in a mammal against  
 CC the above diseases, and for antibody production. AXOR35 nucleotides are  
 CC also useful as diagnostic reagents, in chromosome localisation and tissue  
 CC expression studies, and for producing transgenic animals useful in drug  
 CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35  
 CC protein or fragments thereof, and are also useful for treating conditions  
 CC associated with the expression of the AXOR35 protein. The present  
 CC sequence represents human AXOR35

XX Sequence 390 AA;

Query Match 5.4%; Score 21; DB 4; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLISYDRY 113  
 |||||

Db 93 TDYLLCTASVYNIVLISYDRY 113  
 |||||

RESULT 13

AAM53050

ID AAM53050 standard; protein; 390 AA.

XX AAM53050;

XX 26-MAR-2002 (first entry)

XX Human G protein-coupled receptor nGPCR-2067.

XX Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor;  
 KW signal transduction; mental disorder; central nervous system disease;  
 KW metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder;  
 KW psychotic disorder; Huntington's disease; schizophrenia; migraine;  
 KW depression; anxiety; bipolar disorder; dementia; Alzheimer's disease;  
 KW Parkinson's disease; proliferative disorder; cancer; psoriasis;  
 KW benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia;  
 KW thyroid disorder; cardiovascular disease; hypotension; hypertension;  
 KW thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis;  
 KW inflammatory conditions; autoimmune disorder; rheumatoid arthritis;

KW	hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic; antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic; cardiant; antithaerotic; neuroleptic; antimigraine;
KW	antiparkinsonian; tranquiliser; antidepressant; neuroprotective; anticonvulsant; antiinflammatory; antirheumatic; antiarthritic;
KW	antipsoriatic; gene therapy; receptor.
XX	
OS	Homo sapiens.
XX	
FX	Key
FX	Location/Qualifiers
FX	Domain
FX	19..41
FT	/label= Transmembrane_domain_1
FT	52..74
FT	/label= Transmembrane_domain_2
FT	86..110
FT	/label= Transmembrane_domain_3
FT	128..146
FT	/label= Transmembrane_domain_4
FT	172..194
FT	/label= Transmembrane_domain_5
FT	305..326
FT	/label= Transmembrane_domain_6
FT	342..360
FT	/label= Transmembrane_domain_7
XX	
XX	WO200185793-A2.
PN	
XX	
XX	15-NOV-2001.
PD	
XX	
XX	08-MAY-2001; 2001WO-US014750.
PF	
XX	
XX	08-MAY-2000; 2000US-0203108P.
PR	
XX	
XX	(PHAA ) PHARMACIA & UPJOHN CO.
PA	
XX	
PI	Lind P, Sejltitz T, Vogeli G, Wood LS;
XX	
XX	WPI; 2002-062240/08.
DR	N-PSDB; ABA02496.
DR	
XX	
XX	New polynucleotide, useful for identifying modulator compounds which are used for treating psoriasis, schizophrenia, diabetes, encodes the novel G protein-coupled receptor (ngPCR) polypeptide (ngPCR-2067).
PT	
PT	
XX	
PS	Claim 31; Page 63; 100pp; English.
XX	
CC	This sequence represents a novel human G protein-coupled receptor (GPCR) designated ngPCR-2067. Like all GPCRs, ngPCR-2067 has 7 putative transmembrane domains and is involved in signal transduction. The invention also relates to expression vectors and host cells comprising nucleic acids encoding ngPCR-2067, to recombinant expression of ngPCR-2067, to antibodies specific for ngPCR-2067, to drug screening methods that use ngPCR-2067, and to modulators of ngPCR-2067 activity. ngPCR-2067 nucleic acid sequences may be used to isolate ngPCR-2067 allelic variants and species homologues and may also be used in genetic mapping. The invention also discloses the use of ngPCR-2067 nucleic acids in screening for a predisposition to ngPCR-2067-associated hereditary mental disorders, or for the diagnosis of these disorders. ngPCR-2067 nucleic acids may additionally be used to generate transgenic animals, including knockout animals, which may provide an insight into treating a variety of human disorders, and may also be used in the design of antisense molecules for suppressing expression of ngPCR-2067 in cells. ngPCR-2067, and ngPCR-2067 modulators may be used to treat a wide variety of medical conditions, particularly mental disorders, central nervous system diseases, and metabolic diseases. Diseases that may be treated include viral infections, particularly HIV-1 or HIV-2 infections; pain; central nervous system, neurological and psychotic disorders such as Huntington's disease, schizophrenia, migraine, depression, anxiety, bipolar disorder, dementia, Alzheimer's disease, and Parkinson's disease; proliferative disorders such as cancers, benign prostatic hypertrophy and psoriasis; metabolic disorders such as diabetes, dyslipidaemia, obesity, and anorexia; thyroid disorders; cardiovascular diseases such as hypotension, hypertension, thrombosis, myocardial infarction, cardiomyopathies, and

CC atherosclerosis; inflammatory conditions; autoimmune disorders (e.g.,  
CC rheumatoid arthritis); hormonal disorders; and renal failure  
XX  
SQ Sequence 390 AA;

Query Match 5.4%; Score 21; DB 5; Length 390;  
Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 TDYLLCTASVYNIVLISYDRY 113  
|||||  
Db 93 TDYLLCTASVYNIVLISYDRY 113

RESULT 14  
ABP98629  
ID ABP98629 standard; protein; 390 AA.  
XX AC  
XX AC  
XX AC  
XX 13-JUN-2003 (first entry)  
XX  
XX Human histamine receptor SP9144.  
DE  
XX human; histamine receptor; chromosome 18; anti-inflammatory;  
KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;  
KW anti-migraine; cardiant; anti-rheumatic; anti-arthritic; antipsoriatic;  
KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;  
KW myocardial infarction; migraine; chronic obstructive pulmonary disease;  
KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;  
KW psoriasis; receptor.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US6204017-B1.  
PN  
XX  
PD 20-MAR-2001.  
XX  
XX 07-OCT-1999; 99US-00414010.  
PF  
XX 07-OCT-1999; 99US-00414010.  
PR  
XX (SCHE ) SCHERING CORP.  
FA  
XX Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;  
PI wang S;  
FI  
XX  
XX WPI: 2002-442063/47.  
DR N-PSDB; ABZ80663.  
XX  
XX New nucleic acid encoding antigenic part of human histamine receptor,  
PT useful for preparing antibodies, e.g. for treating-histamine related  
PT disorders.  
XX  
XX Example 1; Col 27-30; 19pp; English.  
PS  
XX  
XX This sequence represents the amino acid sequence of a human histamine  
CC receptor (HR) designated SP9144. The sequence was isolated by searching  
CC databases with the sequence of known G-coupled protein receptor (GPCR).  
CC The gene is used for recombinant production of HR and for preparing  
CC antibodies (Ab). These Ab are used to purify HR by immunoaffinity  
CC chromatography, in immunoassay of histamine receptor, to identify cDNA  
CC clones that express the receptor, as antagonist to block binding of  
CC histamine (for treating any histamine-associated disorder) and to  
CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR  
CC protein can be used in the treatment of e.g. inflammation, asthma,  
CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,  
CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple  
CC sclerosis, inflammatory bowel disease and psoriasis  
XX  
XX Sequence 390 AA;

Query Match 5.4%; Score 21; DB 5; Length 390;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





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# OM protein - protein search, using sw model

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(without alignments)  
630.805 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 391

Sequence: 1 MSNSTGTGILPPAAQVPLAF.....WKILCVTKPALSQNSQSVSS 391

## Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	5.4	390	3	US-09-414-010-2
2	21	5.4	390	4	US-09-812-216-2
3	11	2.8	19	2	US-08-985-090-8
4	11	2.8	19	3	US-09-165-543-8
5	11	2.8	19	3	US-09-165-543-15
6	11	2.8	351	4	US-09-524-162-2
7	11	2.8	445	2	US-08-985-090-2
8	11	2.8	445	3	US-09-165-543-2
9	11	2.8	445	3	US-09-165-543-5
10	11	2.8	445	3	US-09-167-354-7
11	11	2.8	445	4	US-09-642-855-7
12	11	2.8	445	4	US-09-642-514-7
13	9	2.3	362	2	US-08-985-090-5
14	9	2.3	362	3	US-09-165-543-32
15	9	2.3	384	2	US-08-833-226-2
16	8	2.0	252	4	US-09-107-532A-4457
17	7	1.8	22	2	US-08-985-090-9
18	7	1.8	22	2	US-08-985-090-15
19	7	1.8	22	3	US-09-165-543-9
20	7	1.8	22	3	US-09-165-543-16
21	7	1.8	22	3	US-09-165-543-35
22	7	1.8	34	3	US-09-177-249-243
23	7	1.8	57	4	US-09-621-976-5298
24	7	1.8	87	3	US-09-087-232A-18
25	7	1.8	96	4	US-09-489-039A-14289
26	7	1.8	100	3	US-09-087-232A-15
27	7	1.8	110	1	US-08-466-886-32

28 7 1.8 110 3 US-08-469-617-32 Sequence 32, Appl  
29 7 1.8 122 4 US-09-489-039A-8669 Sequence 8669, Ap  
30 7 1.8 146 4 US-09-252-991A-31678 Sequence 31678, A  
31 7 1.8 153 2 US-08-896-365-9 Sequence 9, Appl  
32 7 1.8 184 4 US-08-833-752-4 Sequence 4, Appl  
33 7 1.8 194 4 US-09-489-039A-9376 Sequence 9376, Ap  
34 7 1.8 212 2 US-08-753-159A-4 Sequence 4, Appl  
35 7 1.8 212 3 US-09-133-735-4 Sequence 4, Appl  
36 7 1.8 215 3 US-09-087-232A-17 Sequence 17, Appl  
37 7 1.8 215 4 US-08-833-752-6 Sequence 6, Appl  
38 7 1.8 224 4 US-09-489-039A-8543 Sequence 8543, Ap  
39 7 1.8 233 4 US-09-252-991A-27758 Sequence 27758, A  
40 7 1.8 257 2 US-08-896-365-8 Sequence 8, Appl  
41 7 1.8 260 4 US-09-252-991A-31019 Sequence 31019, A  
42 7 1.8 263 4 US-09-252-991A-30502 Sequence 30502, A  
43 7 1.8 288 2 US-08-466-103A-6 Sequence 6, Appl  
44 7 1.8 329 4 US-09-502-783A-9 Sequence 9, Appl  
45 7 1.8 342 1 US-08-244-646-15 Sequence 15, Appl

## ALIGNMENTS

### RESULT 1

US-09-414-010-2  
; Sequence 2, Application US/09414010  
; Patent No. 6204017

### GENERAL INFORMATION:

; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monsma, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414,010  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-414-010-2

Query Match 5.4%; Score 21; DB 3; Length 390;  
Best Local Similarity 100.0%; Pred. No. 2e-11;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVNVIVLSYDRY 113  
DB 93 TDYLLCTASVNVIVLSYDRY 113

### RESULT 2

US-09-812-216-2  
; Sequence 2, Application US/09812216  
; Patent No. 6613533

### GENERAL INFORMATION:

; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monsma, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/812,216  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 09/414,010

; PRIOR FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-812-216-2

Query Match 5.4%; Score 21; DB 4; Length 390;  
Best Local Similarity 100.0%; Pred. No. 2e-11;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVNVILISYDRY 113  
Db 93 TDYLLCTASVNVILISYDRY 113

## RESULT 3

US-08-985-090-8  
; Sequence 8, Application US/08985090  
; Patent No. 5885693  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl  
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/985,090  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jean M. Silveri  
; REGISTRATION NUMBER: 39,030  
; REFERENCE/DOCKET NUMBER: MNI-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

Query Match 2.8%; Score 11; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.0028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65  
Db 2 LNLAISDFLVG 12

## RESULT 4

US-09-165-543-8  
; Sequence 8, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:

; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-09-165-543-8

Query Match 2.8%; Score 11; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.0028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65  
Db 2 LNLAISDFLVG 12

## RESULT 5

US-09-165-543-15  
; Sequence 15, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780

;  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-09-165-543-15

Query Match 2.8%; Score 11; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.0028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAIISDFLVG 65  
Db 2 LNLAIISDFLVG 12

RESULT 6  
US-09-524-162-2  
; Sequence 2, Application US/09524162  
; Patent No. 6355452  
; GENERAL INFORMATION:  
; APPLICANT: Ping Tsui  
; TITLE OF INVENTION: HUMAN HISTAMINE H3 GENE VARIANT-2  
; FILE REFERENCE: GP-70681  
; CURRENT APPLICATION NUMBER: US/09/524,162  
; CURRENT FILING DATE: 2000-03-13  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-524-162-2

Query Match 2.8%; Score 11; DB 4; Length 351;  
Best Local Similarity 100.0%; Pred. No. 0.037;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAIISDFLVG 65  
Db 74 LNLAIISDFLVG 84

RESULT 7  
US-08-985-090-2  
; Sequence 2, Application US/08985090  
; Patent No. 5885893  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl  
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,090  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jean M. Silveri  
; REGISTRATION NUMBER: 39,030  
; REFERENCE/DOCKET NUMBER: MNI-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-985-090-2

Query Match 2.8%; Score 11; DB 2; Length 445;  
Best Local Similarity 100.0%; Pred. No. 0.045;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAIISDFLVG 65  
Db 74 LNLAIISDFLVG 84

RESULT 8  
US-09-165-543-2  
; Sequence 2, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-165-543-2

Query Match 2.8%; Score 11; DB 3; Length 445;

Best Local Similarity 100.0%; Pred. No. 0.045; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65  
Db 74 LNLAISDFLVG 84

## RESULT 9

US-09-165-543-5  
; Sequence 5, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MMI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-165-543-5

Query Match 2.8%; Score 11; DB 3; Length 445;  
Best Local Similarity 100.0%; Pred. No. 0.045;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65  
Db 74 LNLAISDFLVG 84

## RESULT 10

US-09-167-354-7  
; Sequence 7, Application US/09167354A  
; Patent No. 6136559  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; TITLE OF INVENTION: SUBTYPE  
; FILE REFERENCE: JMW  
; CURRENT APPLICATION NUMBER: US/09/167,354A  
; CURRENT FILING DATE: 1998-10-07

; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE  
US-09-167-354-7

Query Match 2.8%; Score 11; DB 3; Length 445;  
Best Local Similarity 100.0%; Pred. No. 0.045;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65  
Db 74 LNLAISDFLVG 84

## RESULT 11

US-09-642-855-7  
; Sequence 7, Application US/09642855  
; Patent No. 6413743  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; TITLE OF INVENTION: SUBTYPE  
; FILE REFERENCE: JMW  
; CURRENT APPLICATION NUMBER: US/09/642,855  
; CURRENT FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 09/167,354  
; PRIOR FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE  
US-09-642-855-7

Query Match 2.8%; Score 11; DB 4; Length 445;  
Best Local Similarity 100.0%; Pred. No. 0.045;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65  
Db 74 LNLAISDFLVG 84

## RESULT 12

US-09-642-514-7  
; Sequence 7, Application US/09642514  
; Patent No. 6437100  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; TITLE OF INVENTION: SUBTYPE  
; FILE REFERENCE: ORT1290  
; CURRENT APPLICATION NUMBER: US/09/642,514  
; CURRENT FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: US 09/167,354  
; PRIOR FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentn Ver. 2.0  
; SEQ ID NO 7

LENGTH: 445  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE  
US-09-642-514-7

Query Match 2.8%; Score 11; DB 4; Length 445;  
Best Local Similarity 100.0%; Pred. No. 0.045; 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65  
DB 74 LNLAISDFLVG 84

RESULT 13  
US-08-985-090-5  
Sequence 5, Application US/08985090  
Patent No. 5885893  
GENERAL INFORMATION:  
APPLICANT: Andrew D.J. Goodearl  
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,090  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jean M. Silveri  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MNI-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 362 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-985-090-5

Query Match 2.3%; Score 9; DB 2; Length 362;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 NIVLISYDR 112  
DB 41 NIVLISYDR 49

RESULT 14  
US-09-165-543-32  
Sequence 32, Application US/09165543  
Patent No. 6093545  
GENERAL INFORMATION:  
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann  
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor

NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/165,543  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,780  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth A. Hanley  
REGISTRATION NUMBER: 33,505  
REFERENCE/DOCKET NUMBER: MNI-032CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 362 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-165-543-32

Query Match 2.3%; Score 9; DB 3; Length 362;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 NIVLISYDR 112  
DB 41 NIVLISYDR 49

RESULT 15  
US-08-833-226-2  
Sequence 2, Application US/08833226  
Patent No. 5891720  
GENERAL INFORMATION:  
APPLICANT: Moore, Karen  
APPLICANT: Nagle, Deborah  
APPLICANT: Woolf, Elizabeth  
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,226  
FILING DATE: 17-APR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-080  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 384 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-833-226-2

Query Match 2.3%; Score 9; DB 2; Length 384;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NLAISDFLV 64  
Db 94 NLAISDFLV 102

Search completed: October 1, 2004, 10:30:22  
Job time : 33 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:29:06 ; Search time 134 Seconds  
(without alignments)  
938.981 Million cell updates/sec

Title: US-10-626-445-8  
Perfect score: 391  
Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCTKWPALSONQSVSS 391

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1351062 seqs, 321799191 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications\_AA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	5.4	73	10 US-09-782-974C-6	Sequence 6, Appli
2	21	5.4	390	9 US-09-910-411-2	Sequence 2, Appli
3	21	5.4	390	10 US-09-852-165-2	Sequence 2, Appli
4	21	5.4	390	10 US-09-891-138A-6	Sequence 6, Appli
5	21	5.4	390	12 US-10-349-253A-2	Sequence 2, Appli
6	21	5.4	390	12 US-09-875-076-14	Sequence 14, Appl
7	21	5.4	390	12 US-09-876-252-14	Sequence 14, Appl
8	21	5.4	390	13 US-10-052-193-2	Sequence 2, Appli
9	21	5.4	390	14 US-10-225-567A-629	Sequence 629, App
10	21	5.4	390	14 US-10-290-078-27	Sequence 27, Appl
11	21	5.4	390	14 US-10-272-981-14	Sequence 14, Appl
12	21	5.4	390	14 US-10-354-769-2	Sequence 2, Appli
13	21	5.4	390	14 US-10-393-807-14	Sequence 14, Appl
14	21	5.4	390	15 US-10-417-820A-14	Sequence 14, Appl
15	21	5.4	390	16 US-10-696-673-2	Sequence 2, Appli

16	21	5.4	390	16	US-10-723-955-14	Sequence 14, Appl
17	21	5.4	390	16	US-10-737-619-2	Sequence 2, Appli
18	21	5.4	390	16	US-10-782-596-14	Sequence 14, Appl
19	21	5.4	441	16	US-10-398-036-3	Sequence 3, Appli
20	11	2.8	19	9	US-09-350-206-8	Sequence 8, Appli
21	11	2.8	19	9	US-09-350-206-15	Sequence 15, Appl
22	11	2.8	19	9	US-09-349-755-8	Sequence 8, Appli
23	11	2.8	19	9	US-09-349-755-15	Sequence 8, Appli
24	11	2.8	19	9	US-09-166-334-8	Sequence 15, Appl
25	11	2.8	19	9	US-09-166-334-15	Sequence 15, Appl
26	11	2.8	19	14	US-10-282-958-15	Sequence 8, Appli
27	11	2.8	19	14	US-10-282-958-15	Sequence 15, Appl
28	11	2.8	168	10	US-09-791-279-147	Sequence 147, App
29	11	2.8	413	12	US-09-891-053-1	Sequence 1, Appli
30	11	2.8	445	9	US-09-350-206-2	Sequence 2, Appli
31	11	2.8	445	9	US-09-350-206-5	Sequence 5, Appli
32	11	2.8	445	9	US-09-349-755-2	Sequence 2, Appli
33	11	2.8	445	9	US-09-349-755-5	Sequence 5, Appli
34	11	2.8	445	9	US-09-166-334-2	Sequence 2, Appli
35	11	2.8	445	9	US-09-166-334-5	Sequence 5, Appli
36	11	2.8	445	12	US-09-891-053-25	Sequence 25, Appl
37	11	2.8	445	14	US-10-282-958-5	Sequence 5, Appli
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39	11	2.8	445	14	US-10-225-567A-549	Sequence 549, App
40	11	2.8	445	16	US-10-453-106-1	Sequence 2, Appli
41	11	2.8	445	16	US-10-453-106-2	Sequence 2, Appli
42	11	2.8	445	16	US-10-453-106-3	Sequence 3, Appli
43	11	2.8	445	16	US-10-727-021-7	Sequence 7, Appli
44	11	2.8	453	12	US-09-891-053-20	Sequence 20, Appl
45	9	2.3	22	14	US-10-067-649-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1  
US-09-782-974C-6  
; Sequence 6, Application US/09782974C  
; Publication No. US20030082534A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Lind, Peter  
; APPLICANT: Wood, Linda S.  
; APPLICANT: Parodi, Luis A.  
; TITLE OF INVENTION: NO. US20030082534A1el G Protein Coupled Receptor  
; FILE REFERENCE: 411USPHRM311  
; CURRENT APPLICATION NUMBER: US/09/782,974C  
; PRIOR FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 60/165,838  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 09/714,449  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: 60/198,568  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 60/166,071  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/166,678  
; PRIOR FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: 60/173,396  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/184,129  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/185,421  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/185,554  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/185,530  
; PRIOR FILING DATE: 2000-03-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 73

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-6

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Best Local Similarity 100.0%; Pred. No. 3e-12;
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Db 31 TDYLLCTASVYNIVLISYDRY 51

RESULT 2
US-09-910-411-2
; Sequence 2, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiaotong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-910-411-2

Query Match      5.4%; Score 21; DB 9; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 93 TDYLLCTASVYNIVLISYDRY 113

RESULT 3
US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030032784A1 G Protein-Coupled Receptors
; FILE REFERENCE: 002311reqUS
; CURRENT APPLICATION NUMBER: US/09/852,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-165-2

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Best Local Similarity 100.0%; Pred. No. 1.3e-11;
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Db 93 TDYLLCTASVYNIVLISYDRY 113

RESULT 4
US-09-891-138A-6
; Sequence 6, Application US/09891138A
; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1el Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6

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Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 93 TDYLLCTASVYNIVLISYDRY 113

RESULT 5
US-10-349-253A-2
; Sequence 2, Application US/10349253A
; Publication No. US20040043393A1
; GENERAL INFORMATION:
; APPLICANT: Aubart, Kelly
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Graybill, Todd
; APPLICANT: Li, Xiaotong
; APPLICANT: Michalovich, David
; APPLICANT: Morrow, Dwight
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C2
; CURRENT APPLICATION NUMBER: US/10/349,253A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/910,411
; PRIOR FILING DATE: 2001-07-20
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
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; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-349-253A-2

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Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLISYDRY 113  
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Db 93 TDYLLCTASVYNIVLISYDRY 113

## RESULT 6

US-09-875-076-14  
; Sequence 14, Application US/09875076  
; Publication No. US20030017528A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/09/875,076  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
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; PRIOR APPLICATION NUMBER: 60/136,567  
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; PRIOR APPLICATION NUMBER: 60/141,448  
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; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,293  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
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; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 390  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-875-076-14

Query Match 5.4%; Score 21; DB 12; Length 390;  
Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLISYDRY 113  
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Db 93 TDYLLCTASVYNIVLISYDRY 113

## RESULT 7

US-09-876-252-14  
; Sequence 14, Application US/09876252  
; Publication No. US20030018182A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Re  
; FILE REFERENCE: AREN-0054  
; CURRENT APPLICATION NUMBER: US/09/876,252  
; CURRENT FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
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; PRIOR FILING DATE: 1999-03-12  
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; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/152,524  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/151,114  
; PRIOR FILING DATE: 1999-08-27  
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; PRIOR FILING DATE: 1998-11-12  
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; PRIOR FILING DATE: 1999-05-28  
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; PRIOR APPLICATION NUMBER: 60/137,127  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/141,448  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28

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RESULT 11
US-10-272-983-14
; Sequence 14, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Hsin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12

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APPLICANT: Liaw, Chen W.

PRIOR APPLICATION NUMBER: 60/123,945

Mon Oct 4 10:27:26 2004

; PRIOR FILING DATE: 1999-03-12  
 ; PRIOR APPLICATION NUMBER: 60/123,948  
 ; PRIOR FILING DATE: 1999-03-12  
 ; PRIOR APPLICATION NUMBER: 60/123,951  
 ; PRIOR FILING DATE: 1999-03-12  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 155  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 14  
 ; LENGTH: 390  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-417-820A-14

Query Match 5.4%; Score 21; DB 15; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLISYDRY 113  
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 Db 93 TDYLLCTASVYNIVLISYDRY 113

RESULT 15  
 US-10-696-673-2  
 ; Sequence 2, Application US/10696673  
 ; Publication No. US20040105846A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pharmacia & Upjohn Company  
 ; APPLICANT: Lind, Peter  
 ; APPLICANT: Sejlitz, Torsten  
 ; APPLICANT: Vogel, Gabriel  
 ; APPLICANT: Wood, Linda S  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING G PROTEIN-COUPLED RECEPTORS  
 ; FILE REFERENCE: PHRM0025-101/00231REGUS.1 DVI  
 ; CURRENT APPLICATION NUMBER: US/10/696,673  
 ; CURRENT FILING DATE: 2003-10-28  
 ; PRIOR APPLICATION NUMBER: US 60/203,108  
 ; PRIOR FILING DATE: 2000-05-08  
 ; PRIOR APPLICATION NUMBER: US 09/852,165  
 ; PRIOR FILING DATE: 2001-05-08  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 2  
 ; LENGTH: 390  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-696-673-2

Query Match 5.4%; Score 21; DB 16; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLISYDRY 113  
 ||||||||||||||||||  
 Db 93 TDYLLCTASVYNIVLISYDRY 113

Search completed: October 1, 2004, 10:41:05  
 Job time : 135 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:23:00 ; Search time 41 Seconds  
(without alignments)  
917.339 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 391

Sequence: 1 MSESNSTGILLPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: PIR 78:\*  
2: PIR:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	5.4	390	JC7566	histamine H4 recep
2	8	2.0	281	AE3523	icc protein [impor
3	8	2.0	328	T22636	hypothetical prote
4	8	2.0	368	A5450	cysteine synthase
5	8	2.0	400	S64729	protein secretion
6	8	2.0	426	H75578	phenylacetyl-CoA l
7	8	2.0	561	A44128	(N-acetylneuraminy
8	7	1.8	32	B38839	histone H1 - sea u
9	7	1.8	55	AE2381	type I site-specif
10	7	1.8	98	AG1960	hypothetical prote
11	7	1.8	103	H81841	hypothetical prote
12	7	1.8	108	H81098	hypothetical prote
13	7	1.8	111	T16798	hypothetical prote
14	7	1.8	156	I84498	hypothetical prote
15	7	1.8	159	AE3307	melatonin receptor
16	7	1.8	172	D97764	conserved hypothet
17	7	1.8	173	D72586	hypothetical prote
18	7	1.8	212	S13293	hypothetical prote
19	7	1.8	212	A44394	KDEL receptor - hu
20	7	1.8	226	T27286	KDEL receptor - bo
21	7	1.8	228	A29347	hypothetical prote
22	7	1.8	231	D83422	alpha-amylase (EC
23	7	1.8	232	G83609	hypothetical prote
24	7	1.8	254	D84559	probable transcrip
25	7	1.8	257	A36546	probable peptide m
26	7	1.8	271	B35407	unknown protein [i
27	7	1.8	280	D86870	tryptophan synthas
28	7	1.8	308	I50241	hypothetical prote
29	7	1.8	326	T04344	G protein-coupled peroxidase (EC 1.1

#### ALIGNMENTS

##### RESULT 1

JC7566  
histamine H4 receptor, HH4R - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001  
C;Accession: JC7566  
R;Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.  
Biochem. Biophys. Res. Commun. 279, 615-620, 2000  
A;Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.  
A;Reference number: JC7566; MUID: 20568725; PMID:1118334  
A;Contents: Leukocyte  
A;Accession: JC7566  
A;Molecule type: mRNA  
A;Residues: 1-390 <NAK>  
A;Cross-references: DDBJ:AB045370  
C;Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled  
C;Genetics:  
A;Gene: hh4r  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 5.4%; Score 21; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 4e-13;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLISDYRY 113  
|||||

Db 93 TDYLLCTASVYNIVLISDYRY 113  
|||||

##### RESULT 2

AE3523  
icc protein [imported] - Brucella melitensis (strain 16M)  
C;Species: Brucella melitensis  
C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 02-Aug-2002  
C;Accession: AE3523  
R;DelVecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A;Reference number: AD3252; PMID:11756688  
A;Accession: AE3523  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-281 <KUR>  
A;Cross-references: GB:AE008918; PIDN:AAU53352.1; PID:gl7984241; GSPDB:GN00191  
A;Experimental source: strain 16M  
C;Genetics:  
A;Gene: BMEI1011  
A;Map position: II  
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase cpdA; 3',5'-cyclic-nucleotide p  
Query Match 2.0%; Score 8; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 6.4; Mismatches 0; Gaps 0; Indels 0; Gaps 0;

QY 225 ASCHLHRA 232  
Db 191 ASCHLHRA 198

RESULT 3  
T22636  
hypothetical protein F54C9.11 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T22636  
R:Sims, M.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: Z19591  
A:Accession: T22636  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-328 <WIL>  
A:Cross-references: EMBL:Z49967; PIDN:CAA90256.1; GSPDB:GN00020; CESP:F54C9.11  
C:Genetics:  
A:Gene: CESP:F54C9.11  
A:Map position: 2  
A:Introns: 24/2; 92/3

Query Match 2.0%; Score 8; DB 2; Length 328; Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Gaps 0; Indels 0;

QY 219 STTSSAS 226  
Db 29 STTSSAS 36

RESULT 4  
A55450  
cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach  
C:Species: Spinacia oleracea (spinach)  
C:Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 20-Jun-2000  
C:Accession: A55450  
R:Saio, K.; Tatsuguchi, K.; Takagi, Y.; Murakoshi, I.  
J. Biol. Chem. 269, 28187-28192, 1994  
A:Title: Isolation and characterization of cDNA that encodes a putative mitochondrial-located cysteine synthase C #status predicted <MAT>  
A:Reference number: A55450; MUID:95050598; PMID:7961755  
A:Accession: A55450  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-368 <SAI>  
A:Cross-references: GB:D37963; NID:g1066152; PIDN:BAA07177.1; PID:g1066153  
C:Superfamily: threonine dehydratase  
C:Keywords: carbon-oxygen lyase; cysteine biosynthesis; mitochondrion; phosphoprotein; F;1-33/Domain: transit peptide (mitochondrion) #status predicted <TTP>  
F;34-368/Product: cysteine synthase C #status predicted <MAT>  
F;90/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 2.0%; Score 8; DB 2; Length 368; Best Local Similarity 100.0%; Pred. No. 8.2; Mismatches 0; Gaps 0; Indels 0;

QY 218 FSTTSSA 225  
Db 26 FSTTSSA 33

RESULT 5  
S64729  
protein secretion protein xcpS - Pseudomonas putida  
C:Species: Pseudomonas putida  
C:Date: 06-Dec-1996 #sequence\_revision 06-Dec-1996 #text\_change 21-Jul-2000  
C:Accession: S64729; S47506

R:de Groot, A.; Krijger, J.J.; Filloux, A.; Tommassen, J.  
Mol. Gen. Genet. 250, 491-504, 1996  
A:Title: Characterization of type II protein secretion (xcp) genes in the plant growth-stimulating bacterium *Deinococcus radiodurans* R1  
A:Reference number: S64724; MUID:96186881; PMID:8602167  
A:Accession: S64729  
A:Molecule type: DNA  
A:Residues: 1-400 <DEG>  
A:Cross-references: EMBL:X81085; NID:g3293032; PIDN:CAA56981.1; PID:g531742  
C:Genetics:  
A:Gene: xcpS  
C:Superfamily: secretion protein xcpS

Query Match 2.0%; Score 8; DB 2; Length 400; Best Local Similarity 100.0%; Pred. No. 8.8; Mismatches 0; Gaps 0; Indels 0;

QY 303 LARSLAIL 310  
Db 268 LARSLAIL 275

RESULT 6  
H75578  
phenylacetyl-CoA ligase - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C:Accession: H75578  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567286  
A:Accession: H75578  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-426 <WHI>  
A:Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12384.1; PID:g646067  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DRA0256  
A:Map position: 2  
C:Superfamily: coenzyme F390 synthetase II

Query Match 2.0%; Score 8; DB 2; Length 426; Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Gaps 0; Indels 0;

QY 284 SESALRQ 291  
Db 377 SESALRQ 384

RESULT 7  
A44128  
(N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase (EC 2 C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 28-Jul-2003  
C:Accession: A44128  
R:Nagata, Y.; Yamashiro, S.; Yodoi, J.; Lloyd, K.O.; Shiku, H.; Furukawa, K.  
J. Biol. Chem. 267, 12082-12089, 1992  
A:Title: Expression cloning of beta 1,4 N-acetylgalactosaminyltransferase cDNAs that detect  
A:Reference number: A44128; MUID:92291088; PMID:1601877  
A:Accession: A44128  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-561 <NAG>  
A:Experimental source: NK-like cell line YT  
C:Superfamily: (N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase  
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 2.0%; Score 8; DB 1; Length 561;



Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 STSSAS 226  
|||||  
Db 419 STSSAS 426

RESULT 8  
B38839  
histone H1 - sea urchin (Strongylocentrotus intermedius) (fragment)  
C:Species: Strongylocentrotus intermedius  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 12-Apr-1995  
R:Suzuki, M.; Sugitara, M.; Ebashi, S.  
J. Biochem. 108, 347-355, 1990  
A:Title: Sea urchin protease specific to the SPKK motif in histone.  
A:Reference number: P90145; MUID:91115778; PMID:2126010  
A:Accession: B38839  
A:Molecule type: Protein  
A:Residues: 1-32 <SU>  
C:Superfamily: histone H1  
C:Keywords: chromosomal protein; nucleosome

Query Match 1.8%; Score 7; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 9.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 SPRKSS 260  
|||||  
Db 22 SPRKSS 28

RESULT 9  
AE2381  
type I site-specific deoxyribonuclease chain R [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AE2381  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AE2381  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-55 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA000019; PID:gl7133742; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: asr4605

Query Match 1.8%; Score 7; DB 2; Length 55;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 ALSQNS 388  
|||||  
Db 9 ALSQNS 15

RESULT 10  
AG1960  
hypothetical protein asr1234 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AG1960  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AG1960  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-98 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA000019; PID:gl7130581; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: asr1234

Query Match 1.8%; Score 7; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 LTITML 183  
|||||  
Db 32 LTITML 38

## RESULT 11

H81841  
hypothetical protein NMA1503 [imported] - Neisseria meningitidis (strain Z2491 serogroup  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: H81841  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:2022556; PMID:10761919  
A:Accession: H81841  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-103 <PAR>  
A:Cross-references: GB:AL162756; GB:AL157959; MID:97380091; PIDN:CAB84735.1; PID:97380150  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1503  
C:Superfamily: Neisseria meningitidis hypothetical protein NMA1503

Query Match 1.8%; Score 7; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 LAILLSA 313  
|||||  
Db 2 LAILLSA 8

## RESULT 12

H81098  
hypothetical protein NMB1293 [imported] - Neisseria meningitidis (strain MCS8 serogroup F  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: H81098  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiugnani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.  
A:Reference number: A81000; MUID:20175755; PMID:10710307  
A:Accession: H81098  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-108 <TET>  
A:Cross-references: GB:AE002478; GB:AE002098; MID:97226533; PIDN:AAF41669.1; PID:97226534  
A:Experimental source: serogroup B, strain MCS8  
C:Genetics:  
A:Gene: NMB1293  
C:Superfamily: Neisseria meningitidis hypothetical protein NMA1503

Mon Oct 4 10:27:26 2004

Query Match 1.8%; Score 7; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 307 LAILLSA 313  
 |||||  
 Db 7 LAILLSA 13

## RESULT 13

Ti6798  
 hypothetical protein T04A6.1 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C;Accession: T16798  
 R;Vaudin, M.; Anderson, K.  
 submitted to the EMBL Data Library, April 1994  
 A;Description: The sequence of C. elegans cosmid T04A6.  
 A;Reference number: Z18579  
 A;Accession: T16798  
 A;Status: preliminary; translated from GB/EMBL/DBDJ  
 A;Molecule type: DNA  
 A;Residues: 1-111 <VAU>  
 A;Cross-references: EMBL:U00042; NID:g470332; PID:g470333; PIDN:AAA50672.1; CESP:T04A6.1  
 A;Experimental source: strain Bristol N2  
 C;Genetics:  
 A;Gene: CESP:T04A6.1  
 A;Introns: 11/3; 82/1

Query Match 1.8%; Score 7; DB 2; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 LPVISVA 193  
 |||||  
 Db 25 LPVISVA 31

## RESULT 14

I84498  
 melatonin receptor - striped hairy-footed hamster (fragment)  
 C;Species: Phodopus sungorus (striped hairy-footed hamster)  
 C;Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 20-Apr-2000  
 C;Accession: I84498  
 R;Reppert, S.M.; Weaver, D.R.; Ebisawa, T.  
 Neuron 13, 1177-1185, 1994  
 A;Title: Cloning and characterization of a mammalian melatonin receptor that mediates re  
 A;Reference number: I38848; MUID:95033233; PMID:7946354  
 A;Accession: I84498  
 A;Status: preliminary; translated from GB/EMBL/DBDJ  
 A;Molecule type: mRNA  
 A;Residues: 1-156 <RES>  
 A;Cross-references: EMBL:U14110; NID:g602133; PID:g602134  
 C;Superfamily: vertebrate rhodopsin

Query Match 1.8%; Score 7; DB 2; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 FAICWAP 320  
 |||||  
 Db 121 FAICWAP 127

## RESULT 15

A83307  
 conserved hypothetical protein PA2713 [imported] - Pseudomonas aeruginosa (strain PA01)  
 C;Species: Pseudomonas aeruginosa  
 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C;Accession: A83307  
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
 .; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000  
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
 A;Reference number: A82950; MUID:20437337; PMID:10984043  
 A;Accession: A83307  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-159 <STO>  
 A;Cross-references: GB:AE004699; GB:AE004091; NID:g9948782; PIDN:AAG06101.1; GSPDB:GN001;  
 A;Experimental source: strain PA01  
 C;Genetics:  
 A;Gene: PA2713

Query Match 1.8%; Score 7; DB 2; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 ARSLAIL 310  
 |||||  
 Db 14 ARSLAIL 20

Search completed: October 1, 2004, 10:29:45  
 Job time : 43 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:13:35 ; Search time 25 Seconds  
(without alignments)  
814.377 Million cell updates/sec

Title: US-10-626-445-8  
Perfect score: 391  
Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPAISONQSVSS 391

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	5.4	390	1 HH4R HUMAN	Q9h3n8 homo sapien
2	11	2.8	445	1 HH3R CAVPO	Q9j135 cavia porce
3	11	2.8	445	1 HH3R HUMAN	Q9ysn1 homo sapien
4	11	2.8	445	1 HH3R MOUSE	P58406 mus musculus
5	11	2.8	445	1 HH3R RAT	Q9gyn8 rattus norv
6	9	2.3	309	1 CLT2 RAT	Q924t9 rattus norv
7	9	2.3	381	1 PKR2 MOUSE	Q8k458 mus musculus
8	9	2.3	383	1 PKR2 RAT	Q8r415 rattus norv
9	9	2.3	384	1 PKR2 BOVIN	Q8spn1 bos taurus
10	9	2.3	384	1 PKR2 HUMAN	Q8nfj6 homo sapien
11	9	2.3	393	1 PKR1 BOVIN	Q8spn2 bos taurus
12	9	2.3	393	1 PKR1 HUMAN	Q8tcw9 homo sapien
13	9	2.3	393	1 PKR1 MOUSE	Q9jkl1 mus musculus
14	9	2.3	393	1 PKR1 RAT	Q8r416 rattus norv
15	8	2.0	378	1 OPSD CAMAB	Q17292 camponotus
16	8	2.0	378	1 OPSD CARBO	Q17296 cataglyphis
17	8	2.0	640	1 PLB XLULA	Q59863 kluyveromyc
18	7	1.8	153	1 ML13 BRARE	P51049 brachydanio
19	7	1.8	154	1 ML1A PIG	Q02781 sus scrofa
20	7	1.8	173	1 CLF8 MOUSE	Q8czr4 mus musculus
21	7	1.8	202	1 RNFG BUCAP	Q8kai8 buchnera ap
22	7	1.8	212	1 ER21 BOVIN	P24390 homo sapien
23	7	1.8	212	1 ER21 HUMAN	Q02769 bos taurus
24	7	1.8	257	1 ML1A BOVIN	P16608 thermus the
25	7	1.8	271	1 TRPA TETH	P32250 gallus gall
26	7	1.8	308	1 P2Y5 CHICK	P35334 phaseolus v
27	7	1.8	342	1 PG11 PHAVU	P58823 phaseolus v
28	7	1.8	342	1 PG13 PHAVU	Q95n03 sus scrofa
29	7	1.8	345	1 CLT2 PIG	Q9ns75 homo sapien
30	7	1.8	346	1 CLT2 HUMAN	P48039 homo sapien
31	7	1.8	350	1 ML1A HUMAN	P56493 cercopithec
32	7	1.8	352	1 CKR5 CERAE	Q9tw42 cercopithec
33	7	1.8	352	1 CKR5_CERP	

34 7 1.8 352 1 CKR5\_CERTO O62743 cercocebus  
35 7 1.8 352 1 CKR5\_GORGO P56439 gorilla gor  
36 7 1.8 352 1 CKR5\_HUMAN P51681 homo sapien  
37 7 1.8 352 1 CKR5\_HYLLE Q97883 hylobates l  
38 7 1.8 352 1 CKR5\_HYLMU Q95nc0 hylobates m  
39 7 1.8 352 1 CKR5\_HYLSY Q95nc5 hylobates s  
40 7 1.8 352 1 CKR5\_MACMU P79436 macaca mulla  
41 7 1.8 352 1 CKR5\_PANTR P56440 pan troglod  
42 7 1.8 352 1 CKR5\_PAPHA P56441 papio hamad  
43 7 1.8 352 1 CKR5\_PONPY Q97881 pongo pygma  
44 7 1.8 352 1 CKR5\_PYGBI Q97880 pygathrix b  
45 7 1.8 352 1 CKR5\_PYGNE Q97882 pygathrix n

## ALIGNMENTS

RESULT 1  
ID HH4R HUMAN STANDARD; PRT; 390 AA.  
AC Q9H3N8; Q9GZQ0;  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105)  
DE (GPCR105) (SP9144) (AXOR35).  
GN HRH4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20538417; PubMed=10973974;  
RA Oda T., Morikawa N., Saito Y., Masuho Y., Matsumoto S.-I.;  
RT "Molecular cloning and characterization of novel type of histamine  
receptor preferentially expressed in leukocytes.";  
RL J. Biol. Chem. 275:36781-36786(2000).  
RN [2]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RX TISSUE=Leukocyte;  
RC MEDLINE=20568725; PubMed=11118334;  
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;  
RT "Molecular cloning and characterization of a new human histamine  
receptor, HH4R.";  
RL Biochem. Biophys. Res. Commun. 279:615-620(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Jones P.G., Wu S., Betty M.;  
RT "Cloning of a novel histamine receptor.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RX TISSUE=Bone marrow;  
RC PubMed=11179434;  
RA Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.L., Blevitt J.,  
Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.;  
RT "Cloning and pharmacological characterization of a fourth histamine  
receptor (H4) expressed in bone marrow.";  
RL Mol. Pharmacol. 59:420-426(2001).  
RN [5]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RX TISSUE=Eosinophil;  
RC MEDLINE=21104636; PubMed=11181941;  
RA Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A.,  
Anthes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,  
Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,  
Monsma F.J. Jr.;  
RT "Cloning and characterization of a novel human histamine receptor.";  
RL J. Pharmacol. Exp. Ther. 296:1058-1066(2001).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21106320; PubMed=11179436;

Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J., Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L., Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S., Bergsma D.J., Fitzgerald L.R.; and Pharmacological characterization of a novel "Cloning, expression, and pharmacological characterization of a novel human histamine receptor." Mol. Pharmacol. 59:434-441(2001).

[7] SEQUENCE FROM N.A.

RA O'Reilly M.A.; "Identification of a histamine H4 receptor on human eosinophils - Role in eosinophil chemotaxis." Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

[8] SEQUENCE FROM N.A.

RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.; "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center ([www.cdna.org](http://www.cdna.org))."; Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RL FUNCTION: The H4 subclass of histamine receptors could mediate the histamine signals in peripheral tissues. Displays a significant level of constitutive activity (spontaneous activity in the absence of agonist).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and eosinophils. Shows preferential distribution in cells of immunological relevance such as T-cells, dendritic cells, monocytes, mast cells, neutrophils. Also expressed in a wide variety of peripheral tissues, including the heart, kidney, liver, lung, pancreas, skeletal muscle, prostate, small intestine, spleen, fetal liver and lymph node.

CC -1- INDUCTION: Expression is either up-regulated or down-regulated upon activation of the lymphoid tissues and this regulation may depend on the presence of IL-10 or IL-13.

CC -1- MISCELLANEOUS: Does not bind diphenhydramine, lorazepam, ranitidine, cimetidine and chlorpheniramine. Shows modest affinity for dimaprit, imipramine, clobenpropit, thioeramide, burimamide, clozapine, imipip and imetit. The order of inhibitory activity was imetit > clobenpropit > burimamide > thioeramide. Clobenpropit behaves as a partial agonist, dimaprit and imipramine show some agonist activity while clozapine behaves as a full agonist. Thioeramide shows inverse agonism (enhances CAMP activity). The order of inhibitory activity of histamine derivatives was Histamine > N-alpha-methylhistamine > R(-)-alpha-methylhistamine > S(+)-alpha-methylhistamine. Both N-alpha-methylhistamine > R(-)-alpha-methylhistamine behave as full agonists.

CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL; AB044934; BAB13698.1; -

CC EMBL; AB045370; BAB20091.1; -

CC EMBL; AF307973; AAG32052.1; -

CC EMBL; AF312230; AAK12081.1; -

CC EMBL; AF329449; AAK43542.1; -

CC EMBL; AF325356; AAL01684.1; -

CC EMBL; AJ298292; AAC83493.1; -

CC EMBL; AJ136745; AAN01271.1; -

CC PIR; JC7566; JC7566.

CC Genew; HGNC:17383; HRH4.

CC MIM; 606792; -

CC GO; GO:0016021; C:integral to membrane; NAS.

CC GO; GO:0004969; F:histamine receptor activity; NAS.

CC InterPro; IPR000276; GPCR\_Rhodopsin.

CC InterPro; IPR006102; Histamine\_H4.

CC Pfam; PF00001; 7tm\_1; 1.

PRINTS; PR00237; GPCRHHODPSN.

DR PRINTS; PR01726; HISTAMINEH4R.

DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.

DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.

DR G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Lipoprotein; Palmitate.

FT DOMAIN 1 19 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 20 40 1 (POTENTIAL).

FT DOMAIN 41 52 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 53 73 2 (POTENTIAL).

FT DOMAIN 74 87 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 88 108 3 (POTENTIAL).

FT DOMAIN 109 131 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 132 152 4 (POTENTIAL).

FT DOMAIN 153 172 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 173 193 5 (POTENTIAL).

FT DOMAIN 194 304 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 305 325 6 (POTENTIAL).

FT DOMAIN 326 341 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 342 362 7 (POTENTIAL).

FT DOMAIN 363 390 CYTOPLASMIC (POTENTIAL).

FT DISULFID 87 164 BY SIMILARITY.

FT CARBOHYD 5 9 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT LIPID 374 374 S-palmitoyl cysteine (POTENTIAL).

FT CONFLICT 138 138 A -> V (IN REF. 1).

FT CONFLICT 206 206 H -> R (IN REF. 1).

FT CONFLICT 253 253 Q -> R (IN REF. 1).

SQ SEQUENCE 390 AA; 44495 MW; C986B8AE7FF912C3 CRC64;

Query Match 5.48; Score 21; DB 1; Length 390;

Best Local Similarity 100.0%; Pred. No. 2e-13;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVNVIVLISVDYR 113

DB 93 TDYLLCTASVNVIVLISVDYR 113

RESULT 2

HH3R\_CAVPO STANDARD; PRT; 445 AA.

AC Q9JUI35; Q9JUI36; 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Histamine H3 receptor (HH3R).

GN HRH3.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

OX NCBI\_TaxID=10141;

RP [1] SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).

TX TISSUE=Brain;

RC MEDLINE=2018440; PubMed=10757514;

RA Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Pillot C., Cochois V., Schwartz J.-C., Arrang J.-M.;

RT "Cloning and cerebral expression of the guinea pig histamine H3 receptor: evidence for two isoforms."

RL NeuroReport 11:755-759(2000).

CC -1- FUNCTION: The H3 subclass of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylyate cyclase and displays high constitutive activity (spontaneous activity in the absence of agonist).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Long; Synonyms=H3L;

CC IsoId=Q9JUI35-1; Sequence=Displayed;

CC Name=Short; Synonyms=H3S;

CC IsoId=Q9JUI35-2; Sequence=VSP\_001880;

CC -!- TISSUE SPECIFICITY: Expressed widely and abundantly throughout the  
 CC brain. Highly expressed in discrete neuronal populations such as  
 CC pyramidal cells in cerebral cortex or cerebellar purkinje cells.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF267537; AAF78947.1; -;  
 CC EMBL: AF267538; AAF78950.1; -;  
 CC InterPro: IPR000276; GPCR\_Rhodopsin.  
 CC DR Pfam: PF00001; 7tm 1; 1.  
 CC DR PRINTS: PR00237; GPCRHOPOPSN.  
 CC DR PRINTS: PR01471; HISTAMINEH3R.  
 CC DR PROSITE: PS00237; G PROTEIN RECP F1.1; 1.  
 CC DR PROSITE: PS00262; G PROTEIN RECP F1.2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Alternative splicing.  
 FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 41 61 POTENTIAL.  
 FT DOMAIN 62 71 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 72 92 POTENTIAL.  
 FT DOMAIN 93 109 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 110 130 POTENTIAL.  
 FT DOMAIN 131 157 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 158 178 POTENTIAL.  
 FT DOMAIN 179 197 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 198 218 POTENTIAL.  
 FT DOMAIN 219 359 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 360 380 POTENTIAL.  
 FT DOMAIN 381 398 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 399 419 POTENTIAL.  
 FT DOMAIN 420 445 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 20 24 POLY-ALA.  
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPPLIC 276 305 Missing (in isoform Short).  
 FT SQ SEQUENCE 445 AA; 48734 MW; BAE206A3887189A0 CRC64;  
 Query Match 2.8%; Score 11; DB 1; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 0.0042;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 55 LNLAISDFLVG 65  
 Db 75 LNLAISDFLVG 85  
 |||||  
 [1]  
 RESULT 3  
 H3R HUMAN STANDARD; PRT; 445 AA.  
 ID H3R HUMAN Q95NT1; Q9GX22; Q9H4K3;  
 AC Q95NT1; Q9GX22; Q9H4K3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Histamine H3 receptor (H3R) (G protein-coupled receptor 97).  
 GN H3R OR GPCR97.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Thalamus;  
 RX MEDLINE=99278519; PubMed=10347254;  
 RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,  
 RA Huvar A., Jackson M.R., Belander M.G.;

RT "Cloning and functional expression of the human histamine H3  
 RL receptor.";  
 RL Mol. Pharmacol. 55:1101-1107(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.  
 RX MEDLINE=20568725; PubMed=1118334;  
 RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;  
 RT "Molecular cloning and characterization of a new human histamine  
 RL receptor, HH4R.";  
 RL Biochem. Biophys. Res. Commun. 279:615-620(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6 AND 7).  
 RC TISSUE=Thalamus;  
 RX MEDLINE=21181559; PubMed=11284713;  
 RA Coge F., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P.,  
 RA Macia C., Ouvre C., Nagel N., Rigue H., Boutin J.A., Galizzi J.-P.;  
 RT "Genomic organization and characterization of splice variants of the  
 RL human histamine H3 receptor.";  
 RL Biochem. J. 355:279-288(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME  
 RC VAL-280.  
 RX MEDLINE=21953383; PubMed=11956964;  
 RA Wiedemann P., Boenisch H., Oerters F., Bruess M.;  
 RT "Structure of the human histamine H3 receptor gene (HRH3) and  
 RL identification of naturally occurring variations.";  
 RL J. Neural Transm. 109:443-453(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RA Ullner C., Zirwes E., Lubbert H.;  
 RT "Cloning and functional expression of the human histamine H3S  
 RL receptor.";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharasath M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the  
 CC histamine signals in CNS and peripheral nervous system. Signals  
 CC through the inhibition of adenylyl cyclase and displays high  
 CC constitutive activity (spontaneous activity in the absence of  
 CC agonist). Agonist stimulation of isoform 3 neither modified  
 CC adenylyl cyclase activity nor induced intracellular calcium  
 CC mobilization.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS;

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CC Event-Alternative splicing; Named isoforms=7;
CC Comment-Additional isoforms seem to exist;
CC Name=1;
CC IsoId=Q9Y5N1-1; Sequence=VSP_001886;
CC Name=2;
CC IsoId=Q9Y5N1-2; Sequence=VSP_001886;
CC Name=3; Synonym=H3S;
CC IsoId=Q9Y5N1-3; Sequence=VSP_001885;
CC Name=4;
CC IsoId=Q9Y5N1-4; Sequence=VSP_001881;
CC Name=5;
CC IsoId=Q9Y5N1-5; Sequence=VSP_001882;
CC Name=6;
CC IsoId=Q9Y5N1-6; Sequence=VSP_001883;
CC Name=7;
CC IsoId=Q9Y5N1-7; Sequence=VSP_001884;
CC -!- TISSUE SPECIFICITY: Expressed predominantly in the CNS, with the
CC greatest expression in the thalamus and caudate nucleus. The
CC various isoforms are mainly coexpressed in brain, but their
CC relative expression level varies in a region-specific manner.
CC Isoforms 3 and 7 are highly expressed in the thalamus, caudate
CC nucleus and cerebellum while isoforms 5 and 6 show a poor
CC expression. Isoforms 5 and 6 show a high expression in the
CC amygdala, substantia nigra, cerebral cortex and hypothalamus.
CC Isoform 7 is not found in hypothalamus or substantia nigra.
CC -!- DISEASE: Defects in HRH3 are a cause of Shy-Drager syndrome
CC [MIM:146500]. This syndrome is characterized by orthostatic
CC hypotension, bladder and bowel incontinence, anhidrosis, iris
CC atrophy, amyotrophy, ataxia, rigidity and tremor.
CC -!- MISCELLANEOUS: Does not bind to cinetidine and triptolidine. Shows
CC modest affinity for thioperamide, imetit, N-alpha-methylhistamine
CC and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to
CC iodoproxyfan while isoforms 1 and 3 bind it with high affinity.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF140538; AAD38151.1; -
CC EMBL; AB045369; BAB20030.1; -
CC EMBL; AB019000; BAB17030.1; -
CC EMBL; AJ296652; CAC51025.1; -
CC EMBL; AJ278250; CAC39434.1; -
CC EMBL; AL078633; CAC04014.1; -
CC EMBL; AF363791; AAK50040.1; -
CC GeneW; HGNC:5184; HRH3.
CC MIM; 604525; -
CC MIM; 146500; -
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004969; F:histamine receptor activity; TAS.
CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . . ; TAS.
CC GO; GO:0007269; P:neurotransmitter secretion; TAS.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; -
CC PRINTS; IPR003380; H3_receptor.
CC PRINTS; PR00237; GPCR_RHODPSN.
CC PRINTS; PR01471; HISTAMINEHR3.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Alternative splicing; Disease mutation.
CC DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 40 60 POTENTIAL.
CC DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 71 91 POTENTIAL.
CC DOMAIN 92 108 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 109 129 POTENTIAL.
CC DOMAIN 130 156 CYTOPLASMIC (POTENTIAL).
CC

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FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 196 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 197 217 POTENTIAL.
FT DOMAIN 218 359 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 360 380 POTENTIAL.
FT DOMAIN 381 395 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 396 416 POTENTIAL.
FT DOMAIN 417 445 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 223 POLY-ALA.
FT DOMAIN 250 256 POLY-PRO.
FT DOMAIN 292 298 POLY-GLY.
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 85 98 Missing (in isoform 4).
FT VARSPLIC 197 315 Missing (in isoform 5).
FT VARSPLIC 227 342 Missing (in isoform 6).
FT VARSPLIC 234 263 Missing (in isoform 7).
FT VARSPLIC 274 353 Missing (in isoform 3).
FT VARSPLIC 445 445 K -> KKKKKTKCL (in isoform 2).
FT VARIANT 280 280 A -> V (IN SHY-DRAGER SYNDROME).
FT CONFLICT 19 19 /FTID=VAR_012235.
FT SEQUENCE 445 AA; 48671 MM; 2ACF7440FEE95B6C CRC64;
Query Match 2.8%; Score 11; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 55 LNLAISDFLWG 65
Db 74 LNLAISDFLWG 84
RESULT 4
ID_H3R_MOUSE STANDARD; PRT; 445 AA.
AC P59406;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histamine H3 receptor (HRH3).
GN HRH3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1;
RA Coqe P., Rigue H., Levacher B., Leopold O., Guenin S.-P., Boutin J.A.,
RA Galizzi J.-P.;
RA "Cloning of mouse histamine H3 receptor";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the
CC histamine signals in CNS and peripheral nervous system. Signals
CC through the inhibition of adenylylate cyclase and displays high
CC constitutive activity (spontaneous activity in the absence of
CC agonist) (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC

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CC EMBL; AY044153; AAK72406.1; --
DR MGD; MGI:2139279; Hrb3.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR003980; H3_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR01471; HISTAMINEH3.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 60 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 61 70 POTENTIAL.
FT TRANSMEM 71 91 POTENTIAL.
FT DOMAIN 92 108 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 109 129 POTENTIAL.
FT DOMAIN 130 156 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 196 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 197 217 POTENTIAL.
FT DOMAIN 218 359 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 360 380 POTENTIAL.
FT DOMAIN 381 396 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 397 417 POTENTIAL.
FT DOMAIN 418 445 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 20 23 POLY-ALA.
SQ SEQUENCE 445 AA; 48541 MW; 8BD406E29E1F3C5F CRC64;
Query Match 2.8%; Score 11; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 55 LNLAIISDFLVG 65
Db 74 LNLAIISDFLVG 84
|||||
|||||

RESULT 5
HH3R_RAT
ID HH3R_RAT STANDARD; PRT; 445 AA.
AC Q9QYN8; Q9QYN6; Q9QYN7; Q9QYN9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Histamine H3 receptor (HH3R).
GN HH3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hypothalamus;
RX MEDLINE=20330707; PubMed=10869375;
RA Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;
RT "Cloning of rat histamine H3 receptor reveals distinct species
pharmacological profiles.";
RL J. Pharmacol. Exp. Ther. 293:771-778 (2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Striatum;
RX MEDLINE=21016732; PubMed=11130725;
RA Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,
RA Stark H., Schunack W., Ganellin C.R., Schwartz J.-C., Arrang J.-M.;
RT "High constitutive activity of native H3 receptors regulates histamine
neurons in brain.";
RL Nature 408:860-864 (2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RA Itadani H., Takimura T., Nakamura T., Ohta M.;
RT "Cloning of a novel G protein-coupled receptor.";

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RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=99278519; PubMed=10347254;
RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
RA Huvar A., Jackson M.R., Erlander M.G.;
RT "Cloning and functional expression of the human histamine H3
receptor.";
RL Mol. Pharmacol. 55:1101-1107 (1999).
CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the
histamine signals in CNS and peripheral nervous system. Signals
through the inhibition of adenylyl cyclase and displays high
constitutive activity (spontaneous activity in the absence of
agonist).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=H3L;
CC IsoId=Q9QYN8-1; Sequence=Displayed;
CC Name=2; Synonyms=H3S;
CC IsoId=Q9QYN8-2; Sequence=VSP_001887;
CC Name=3;
CC IsoId=Q9QYN8-3; Sequence=VSP_001888;
CC Name=4;
CC IsoId=Q9QYN8-4; Sequence=VSP_001888, VSP_001889;
CC -!- TISSUE SPECIFICITY: Expressed abundantly in brain, most notably
throughout the thalamus, the ventromedial hypothalamus and the
caudate nucleus. Isoform 1 is largely predominant in all tissues.
CC -!- MISCELLANEOUS: Proxofan acts as a potent neutral antagonist while
thiopramide, ciproxifan and FUB465 act as potent inverse
agonists.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
EMBL; AF237919; AAF82086.1; --
DR EMBL; AY009370; AAK02069.1; --
DR EMBL; AB015646; BAA88765.1; --
DR EMBL; AB015646; BAA88766.1; --
DR EMBL; AB015646; BAA88767.1; --
DR EMBL; AB015646; BAA88768.1; --
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR003980; H3_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR01471; HISTAMINEH3.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
Alternative splicing.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 60 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 61 70 POTENTIAL.
FT TRANSMEM 71 91 POTENTIAL.
FT DOMAIN 92 108 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 109 129 POTENTIAL.
FT DOMAIN 130 156 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 196 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 197 217 POTENTIAL.
FT DOMAIN 218 359 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 360 380 POTENTIAL.
FT DOMAIN 381 396 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 397 417 POTENTIAL.
FT DOMAIN 418 445 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 23 POLY-ALA.

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RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
FT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22389257; PubMed=12477932;  
RA Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Jones S.J.W., Maria M.A.,  
RA Schnerch A., Schein J.E., Kzywinski M.I., Skalska U., Smalus D.E.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Receptor for prokineticin 2. Exclusively coupled to the  
CC G(q) subclass of heteromeric G proteins. Activation leads to  
CC mobilization of calcium, stimulation of phosphoinositide turnover  
CC and activation of p44/p42 mitogen-activated protein kinase (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in several regions of the brain,  
CC including paraventricular hypothalamic nucleus, dorsal medial  
CC hypothalamic nucleus, paratenial thalamic nuclei, paracentral  
CC thalamic nucleus, lateral habenular nucleus, lateral septal  
CC nucleus, lateral globus pallidus and amygdala. Highest expression  
CC seen in paraventricular thalamic nuclei and is also extensively  
CC expressed in the suprachiasmatic nucleus.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: AF487279; AAM49571.1; -  
CC EMBL: AK030458; BAC26971.1; ALT\_INIT.  
CC EMBL: AK041586; BAC30994.1; -  
CC EMBL: AK080980; BAC38103.1; -  
CC EMBL: BC043116; AHA43116.1; -  
CC MGD: MGI:2181363; Gpr73l1.  
CC GO: GO:0007623; P:circadian rhythm; IDA.  
CC InterPro: IPR000276; GPCR\_Rhodpsn.  
CC Pfam: PF00001; 7tm 1; 1.  
CC PRINTS: PR00237; GPCRHOPOPSN.  
CC PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein.  
CC  
CC DOMAIN 1 51  
CC EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 52 72  
CC 1 (POTENTIAL).  
CC DOMAIN 73 86  
CC CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 87 107  
CC 2 (POTENTIAL).  
CC DOMAIN 108 133  
CC EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 134 154  
CC 3 (POTENTIAL).  
CC DOMAIN 155 168  
CC CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 169 189  
CC 4 (POTENTIAL).

FT DOMAIN 190 220  
FT TRANSMEM 221 241  
FT DOMAIN 242 270  
FT TRANSMEM 271 291  
FT DOMAIN 292 310  
FT TRANSMEM 311 331  
FT DOMAIN 332 381  
FT CARBOHYD 7 7  
FT CARBOHYD 24 24  
FT DISULFID 125 245  
FT CONFLICT 244 244  
FT CONFLICT 375 375  
SQ SEQUENCE 381 AA; 43375 MW; 1981FD101324166D CRC64;  
Query Match 2.3%; Score 9; DB 1; Length 381;  
Best Local Similarity 100.0%; Pred. No. 0.41; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Gaps 0;  
QY 56 NLAISDFLV 64  
DB 91 NLAISDFLV 99  
|||||||  
|||||||  
RESULT 8  
PKR2 RAT  
ID PKR2 RAT STANDARD; PRT; 383 AA.  
AC Q8R415;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DE Prokineticin receptor 2 (PK-R2) (G protein-coupled receptor 73-like 1)  
DE (G protein-coupled receptor ISE).  
GN GPR73L1 OR PKR2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=22050031; PubMed=12054613;  
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,  
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,  
RA Inatomi N., Ohtaki T., Onda H., Fujino M.;  
RT "Isolation and identification of EG-VEGF/prokineticins as cognate  
RT ligands for two orphan G-protein-coupled receptors";  
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).  
CC -!- FUNCTION: Receptor for prokineticin 2. Exclusively coupled to the  
CC G(q) subclass of heteromeric G proteins. Activation leads to  
CC mobilization of calcium, stimulation of phosphoinositide turnover  
CC and activation of p44/p42 mitogen-activated protein kinase (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Abundantly expressed in the CNS and  
CC reproductive organs with the highest levels in the cerebellum,  
CC cerebellum, testis and ovary.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC  
CC EMBL: AY089975; AAM1891.1; ALT\_INIT.  
CC InterPro: IPR000276; GPCR\_Rhodpsn.  
CC Pfam: PF00001; 7tm 1; 1.  
CC PRINTS: PR00237; GPCRHOPOPSN.  
CC PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein.  
CC  
CC DOMAIN 1 51  
CC EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 52 72  
CC 1 (POTENTIAL).  
CC DOMAIN 73 86  
CC CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 87 107  
CC 2 (POTENTIAL).  
CC DOMAIN 108 133  
CC EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 134 154  
CC 3 (POTENTIAL).  
CC DOMAIN 155 168  
CC CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 169 189  
CC 4 (POTENTIAL).

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DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1. Glycoprotein.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 53 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 54 74 1 (POTENTIAL).
FT DOMAIN 75 89 2 (POTENTIAL).
FT TRANSMEM 90 110 3 (POTENTIAL).
FT DOMAIN 111 136 4 (POTENTIAL).
FT TRANSMEM 137 157 5 (POTENTIAL).
FT DOMAIN 158 170 6 (POTENTIAL).
FT TRANSMEM 171 191 7 (POTENTIAL).
FT DOMAIN 192 222 8 (POTENTIAL).
FT TRANSMEM 223 243 9 (POTENTIAL).
FT DOMAIN 244 272 10 (POTENTIAL).
FT TRANSMEM 273 293 11 (POTENTIAL).
FT DOMAIN 294 312 12 (POTENTIAL).
FT TRANSMEM 313 333 13 (POTENTIAL).
FT DOMAIN 334 383 14 (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 128 207 BY SIMILARITY.
SQ SEQUENCE 383 AA; 43603 MW; 477C501099535B93 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NLAISDFLV 64
DB 94 NLAISDFLV 102

RESULT 9
PKR2_BOVIN STANDARD; PRT; 384 AA.
AC Q8SPN1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Prokineticin receptor 2 (PK-R2) (G protein-coupled receptor 73-like 1)
DE (G protein-coupled receptor 15E).
GN GPR73L1 OR PKR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=22050031; PubMed=12054613;
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohtaki T., Onda H., Fujino M.;
RA "Isolation and identification of EG-VEGF/prokineticins as cognate
RA ligands for two orphan G-protein-coupled receptors."
RT Biochem. Biophys. Res. Commun. 293:396-402(2002).
CC -!- FUNCTION: Receptor for prokineticin 2. Exclusively coupled to the
CC G(q) subclass of heteromeric G proteins. Activation leads to
CC mobilization of calcium, stimulation of phosphoinositide turnover
CC and activation of p44/p42 mitogen-activated protein kinase (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AY089973; AAML1889.1; -.
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
DR

```

RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Lehaealaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A.C., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.B., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
CC -!- FUNCTION: Receptor for prokineticin 2. Exclusively coupled to the  
CC G(q) subclass of heteromeric G proteins. Activation leads to  
CC mobilization of calcium, stimulation of phosphoinositide turnover  
CC and activation of p44/p42 mitogen-activated protein kinase.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in the ileocecum, thyroid gland,  
CC pituitary gland, salivary gland, adrenal gland, testis, ovary and  
CC brain.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous  
CC gene model prediction.  
CC -----  
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CC -----  
CC EMBL; AF506288; AAM48128.1; -;  
CC EMBL; AB084081; BAC24022.1; -;  
CC EMBL; AL121755; CAB89854.1; ALT\_SEQ.  
CC DR Genbank; HGNC:15836; GPR7311.  
CC MIM; 607123;  
CC InterPro; IPR000276; GPCR\_Rhodpsn.  
CC Pfam; PF00001; 7tm.1; 1.  
CC PRINTS; PR00237; GPCRHHODPSN.  
CC PROSITE; PS00237; G\_PROTEIN\_RECF\_F1\_1; 1.  
CC PROSITE; PS0262; G\_PROTEIN\_RECF\_F2\_1;  
CC G-protein coupled receptor; Transmembrane; Glycoprotein.  
CC DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 55 75 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 76 89 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 111 136 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 137 157 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 158 171 CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 172 192 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 193 223 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 224 244 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 245 273 CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 274 294 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 295 313 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 314 334 EXTRACELLULAR (POTENTIAL).  
CC DOMAIN 335 384 CYTOPLASMIC (POTENTIAL).  
CC CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC DISULFID 128 208 BY SIMILARITY.  
CC SEQUENCE 384 AA; 43995 MW; 2D5BFA3655347B5E CRC64;  
Query Match 2.3%; Score 9; DB 1; Length 384;  
Best Local Similarity 100.0%; Pred. No. 0.41;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 56 NLAISDFLV 64  
DB 94 NLAISDFLV 102  
RESULT 11  
PARI BOVIN  
ID PKR1 BOVIN STANDARD; PRT; 393 AA.  
AC Q8SPN2;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Prokineticin receptor 1 (PK-R1) (G protein-coupled receptor 73)  
DE (G protein-coupled receptor ZAQ).  
DE GPR73 OR PKR1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22050031; PubMed=12054613;  
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,  
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,  
RA Inatomi N., Ohkaki T., Onda H., Fujino M.  
RT "Isolation and identification of EG-VGFP/prokineticins as cognate  
RT ligands for two orphan G-protein-coupled receptors.";  
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).  
CC -!- FUNCTION: Receptor for prokineticin 1. Exclusively coupled to the  
CC G(q) subclass of heteromeric G proteins. Activation leads to  
CC mobilization of calcium, stimulation of phosphoinositide turnover  
CC and activation of p44/p42 mitogen-activated protein kinase (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC -----  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AY089972; AAM11888.1; -;  
CC InterPro; IPR000276; GPCR\_Rhodpsn.  
CC Pfam; PF00001; 7tm.1; 1.  
CC PRINTS; PR00237; GPCRHHODPSN.  
CC PROSITE; PS00237; G\_PROTEIN\_RECF\_F1\_1; 1.  
CC PROSITE; PS0262; G\_PROTEIN\_RECF\_F2\_1;  
CC G-protein coupled receptor; Transmembrane; Glycoprotein.  
CC DOMAIN 1 63 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 64 84 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 85 98 CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 99 119 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 120 145 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 146 166 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 167 179 CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 180 200 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 201 232 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 233 253 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 254 282 CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 283 303 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 304 322 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 323 343 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 344 393 CYTOPLASMIC (POTENTIAL).  
CC CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC DISULFID 137 217 BY SIMILARITY.

```

DR MM: 607122; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR DR PROSITE: PS00262; G_PROTEIN_RECP_F1_2; 1.
DR DR PROSITE: PS00262; G_PROTEIN_RECP_F1_2; 1.
DR KW G-protein coupled receptor; Transmembrane; Glycoprotein.
DR FT DOMAIN 1 62
DR FT TRANSMEM 63 83
DR FT DOMAIN 84 98
DR FT TRANSMEM 99 119
DR FT DOMAIN 120 146
DR FT TRANSMEM 147 167
DR FT DOMAIN 168 180
DR FT TRANSMEM 181 201
DR FT DOMAIN 202 232
DR FT TRANSMEM 233 253
DR FT DOMAIN 254 282
DR FT TRANSMEM 283 303
DR FT DOMAIN 304 322
DR FT TRANSMEM 323 343
DR FT DOMAIN 344 393
DR FT CARBOHYD 11 11
DR FT CARBOHYD 14 14
DR FT CARBOHYD 36 36
DR FT DISULFID 137 217
DR FT CONFLICT 255 256
DR FT CONFLICT 255 256
DR SEQUENCE 393 AA; 44769 MW; 0D36461CA99CAEC1 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NLAISDFLV 64
DB 103 NLAISDFLV 111
|||||||

RESULT 13
PKR1 MOUSE
ID PKR1 MOUSE STANDARD; PRT; 393 AA.
AC Q9JXL1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Prokineticin receptor 1 (PK-R1) (G protein-coupled receptor 73).
DE GPR73 OR PKR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22025484; PubMed=10760605;
RA Parker R., Liu M., Eyre H.J., Copeland N.G., Gilbert D.J.,
RA Crawford J., Sutherland G.R., Jenkins N.A., Herzog H.;
RT "Y-receptor-like genes GPR72 and GPR73: molecular cloning, genomic
RT organisation and assignment to human chromosome 11q21.1 and 2p14 and
RT mouse chromosome 9 and 6.";
RL Biochim. Biophys. Acta 1491:369-375 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=2202134; PubMed=12024206;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus.";
RL Nature 417:405-410 (2002).
CC -!- FUNCTION: Receptor for prokineticin 1. Exclusively coupled to the
CC Gq() subclass of heteromeric G proteins. Activation leads to
CC mobilization of calcium, stimulation of phosphoinositide turnover

```

CC and activation of p44/p42 mitogen-activated protein kinase (By  
CC similarity).  
CC  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC  
CC -!- TISSUE SPECIFICITY: Expressed at high levels in the heart, skeletal  
CC muscle and pancreas. Expressed at lower levels in the brain, lung,  
CC liver and kidney.  
CC  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF236082; AAF43706.1; -  
CC EMBL; AF487278; AAM49570.1; -  
CC MGD; MGI:1929676; Gpr73.  
CC InterPro: IPR000276; GPCR\_Rhodpsn.  
CC Pfam; PF00001; 7tm\_1; 1.  
CC PRINTS; PR00237; GPCRHHODPSN.  
CC PROSITE; PS00237; G PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE; PS0262; G PROTEIN\_RECEP\_F1\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein.  
CC DOMAIN 1 62 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 63 83 1 (POTENTIAL).  
CC DOMAIN 84 98 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 99 119 2 (POTENTIAL).  
CC DOMAIN 120 146 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 147 167 3 (POTENTIAL).  
CC DOMAIN 168 179 3 (POTENTIAL).  
CC TRANSSEM 180 200 4 (POTENTIAL).  
CC DOMAIN 201 232 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 233 253 5 (POTENTIAL).  
CC DOMAIN 254 282 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 283 303 6 (POTENTIAL).  
CC DOMAIN 304 322 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 323 344 7 (POTENTIAL).  
CC DOMAIN 344 393 CYTOPLASMIC (POTENTIAL).  
CC CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC DISULFID 137 217 BY SIMILARITY.  
CC SEQUENCE 393 AA; 44528 MW; 46F5E78C0DDC871C CRC64;

Query Match 2.3%; Score 9; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NLAISDFLV 64  
Db 103 NLAISDFLV 111  
|||||  
STANDARD; PRT; 393 AA.  
RESULT 14  
PKR1 RAT  
ID PKR1 RAT STANDARD; PRT; 393 AA.  
AC Q8B416;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Prokineticin receptor 1 (PK-R1) (G protein-coupled receptor 73)  
DE (G protein-coupled receptor ZAQ).  
GN GPR73 OR PKR1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=22050031; PubMed=12054613;  
RA Masuda Y., Takatsu Y., Teruo Y., Kumano S., Ishibashi Y., Suenaga M.,  
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,

RA Inatomi N., Ohtaki T., Onda H., Fujino M.;  
RT "Isolation and identification of EG-VEGF/prokineticins as cognate  
RL ligands for two orphan G-protein-coupled receptors.";  
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).  
CC -!- FUNCTION: Receptor for prokineticin 1. Exclusively coupled to the  
CC G(q) subclass of heteromeric G proteins. Activation leads to  
CC mobilization of calcium, stimulation of phosphoinositide turnover  
CC and activation of p44/p42 mitogen-activated protein kinase (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Widely expressed in peripheral tissues with  
CC the highest level in the spleen and moderate levels in the adipose  
CC tissues, thymus, lung, kidney, testis, uterus and small intestine.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AY089974; AAM11890.1; -  
CC InterPro: IPR000276; GPCR\_Rhodpsn.  
CC Pfam; PF00001; 7tm\_1; 1.  
CC PRINTS; PR00237; GPCRHHODPSN.  
CC PROSITE; PS00237; G PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE; PS0262; G PROTEIN\_RECEP\_F1\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein.  
CC DOMAIN 1 62 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 63 83 1 (POTENTIAL).  
CC DOMAIN 84 98 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 99 119 2 (POTENTIAL).  
CC DOMAIN 120 145 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 146 166 3 (POTENTIAL).  
CC DOMAIN 167 179 3 (POTENTIAL).  
CC TRANSSEM 180 200 4 (POTENTIAL).  
CC DOMAIN 201 232 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 233 253 5 (POTENTIAL).  
CC DOMAIN 254 282 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 283 303 6 (POTENTIAL).  
CC DOMAIN 304 322 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 323 343 7 (POTENTIAL).  
CC DOMAIN 344 393 CYTOPLASMIC (POTENTIAL).  
CC CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC DISULFID 137 217 BY SIMILARITY.  
CC SEQUENCE 393 AA; 44507 MW; C75EC72B97E503A8 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NLAISDFLV 64  
Db 103 NLAISDFLV 111  
|||||  
STANDARD; PRT; 378 AA.  
RESULT 15  
OPSD CAMAB  
ID OPSD CAMAB STANDARD; PRT; 378 AA.  
AC Q17292;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Rhodopsin.  
OS Camponotus abdominalis (Carpenter ant).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Formicidae; Formicinae; Camponotus.  
OX NCBI\_TaxID=47731;  
RN [1]  
RP SEQUENCE FROM N.A.

Mon Oct 4 10:27:26 2004

```
RC TISSUE=Retina;
RX MEDLINE=98039419; PubMed=9372150;
RA Popp M.P., Grishammer R., Hargrave P.A., Smith W.C.;
RT "Ant opsins: sequences from the Saharan silver ant and the carpenter ant.";
RL Invertebr. Neurosci. 1:323-329(1996).
CC -!- FUNCTION: Visual pigments are the light-absorbing molecules that mediate vision. They consist of an apoprotein, opsin, covalently linked to cis-retinal.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: Some or all of the carboxyl-terminal Ser or Thr residues may be phosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Opsin subfamily.
CC -----
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CC -----
DR ENBL; U32502; AAC47083.1; -.
DR HSP; P02699; IF88.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR InterPro; IPR001760; Opsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECP_Fl_2; 1.
DR PROSITE; PS00238; OPSIN; 1.
DR Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; G-protein coupled receptor.
FT DOMAIN 1 53
FT TRANSMEM 54 78
FT DOMAIN 79 90
FT TRANSMEM 91 115
FT DOMAIN 116 130
FT TRANSMEM 131 150
FT DOMAIN 151 169
FT TRANSMEM 170 193
FT DOMAIN 194 217
FT TRANSMEM 218 245
FT DOMAIN 246 280
FT TRANSMEM 281 304
FT DOMAIN 305 311
FT TRANSMEM 312 336
FT DOMAIN 337 378
FT DISULFID 127 204
FT BINDING 323 323
FT CARBOHYD 24 24
FT CARBOHYD 200 200
SQ SEQUENCE 378 AA; 42091 MW; 99C95CB5093BA433 CRC64;
Query Match 2.0%; Score 8; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 56 NLAISDFL 63
DB 95 NLAISDFL 102
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Search completed: October 1, 2004, 10:26:53  
Job time : 27 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 1, 2004, 10:20:40 ; Search time 118 Seconds  
(without alignments)  
1045.488 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 391

Sequence: 1 MSENSTGILPPAAQVPLAF.....WKILCVTKPALSQNSVSS 391

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mmc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	379	96.9	391	11	Q91ZY2 mus musculus
2	33	8.4	391	11	Q91ZY1 rat mus norv
3	32	8.2	389	11	Q91ZY3 cavia porce
4	21	5.4	390	4	Q96LD9
5	16	4.1	390	6	Q8WNV9
6	11	2.8	147	6	Q865E3
7	11	2.8	200	4	Q8NI50
8	11	2.8	301	4	Q8WY00
9	11	2.8	309	4	Q8NI49
10	11	2.8	365	4	Q8WY01
11	11	2.8	373	4	Q8WY29
12	11	2.8	445	6	Q865E1
13	8	2.0	79	10	Q84PJ1
14	8	2.0	150	2	Q9FL30
15	8	2.0	181	4	Q9BQJ4
16	8	2.0	181	6	Q9XSV3

17	8	2.0	181	11	Q9JJG6
18	8	2.0	278	3	Q871W9
19	8	2.0	281	16	Q8YDR4
20	8	2.0	281	16	Q8FUN6
21	8	2.0	292	16	Q98JZ0
22	8	2.0	314	16	Q8E3K3
23	8	2.0	314	16	Q8DXY4
24	8	2.0	328	5	Q20759
25	8	2.0	368	10	Q43153
26	8	2.0	396	16	Q7WD90
27	8	2.0	396	16	Q7W5Q4
28	8	2.0	396	16	Q7VW94
29	8	2.0	400	2	Q52293
30	8	2.0	400	16	Q88P05
31	8	2.0	426	16	Q9RYQ3
32	8	2.0	457	16	Q7WJ42
33	8	2.0	527	10	Q94HB1
34	8	2.0	534	13	O57422
35	8	2.0	672	10	Q94D59
36	8	2.0	902	5	Q86198
37	8	2.0	1188	16	Q8E9K4
38	8	2.0	9271	5	Q8IES7
39	7	1.8	55	16	Q8YNG1
40	7	1.8	72	6	Q866B5
41	7	1.8	80	4	Q8TDP5
42	7	1.8	82	4	Q8TDP6
43	7	1.8	93	10	Q8H1V0
44	7	1.8	98	16	Q8YXH9
45	7	1.8	100	17	Q8PZT9

#### ALIGNMENTS

#### RESULT 1

Q91ZY2 ID Q91ZY2 PRELIMINARY; PRT; 391 AA.  
AC Q91ZY2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Histamine H4 receptor.  
GN HRH4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
RT "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation."  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AF358859; AAK97380.1; -;  
DR MGD; MGI:2429635; Hrha.  
DR GO; GO:0005887; C:integral to plasma membrane; IC.  
DR GO; GO:0005624; C:membrane fraction; IDA.  
DR GO; GO:0004969; F:histamine receptor activity; IDA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR008102; Histamine\_H4.  
DR Pfam; PF00001; 7tm1; 1.  
DR PRINTS; PR00237; HISTAMINEH4R.  
DR PROSITE; PS00237; G-PROTEIN RECEPT\_F1\_1; 1.  
DR PROSITE; PS00462; G-PROTEIN RECEPT\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 391 AA; 44248 MW; 59EC73CB5214C5E0 CRC64;  
Query Match 96.9%; Score 379; DB 11; Length 391;  
Best Local Similarity 100.0%; Pred. No. 0;

Q9JJG6 mus musculus  
Q871W9 neurospora  
Q8YDR4 bruceella me  
Q8FUN6 bruceella su  
Q98JZ0 rhizobium l  
Q8E3K3 streptococ  
Q8DXY4 streptococ  
Q20759 caenorhabdi  
Q43153 spinacia ol  
Q7WD90 bordetella  
Q7W5Q4 bordetella  
Q7VW94 bordetella  
Q52293 pseudomonas  
Q88P05 pseudomonas  
Q9RYQ3 deinococcus  
Q7WJ42 bordetella  
Q94HB1 oryza sativ  
O57422 xenopus lae  
Q94D59 oryza sativ  
Q86198 dictyosteli  
Q8E9K4 shewanella  
Q8IES7 plasmodium  
Q8YNG1 anabaena sp  
Q866B5 cebus apell  
Q8TDP5 homo sapien  
Q8TDP6 homo sapien  
Q8H1V0 mirabilis j  
Q8YXH9 anabaena sp  
Q8PZT9 methanosarc

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSESNTGILPPAAQVFLAFIMSSFAFAMVGNVAVILAFVVDRLNHRSNYFFLNLAIS 60  
 DB 1 MSESNTGILPPAAQVFLAFIMSSFAFAMVGNVAVILAFVVDRLNHRSNYFFLNLAIS 60

QY 61 DFLVGLISIPLYIPIHVLFWNNFGSGICMFWLITDYLCTASVYVNLISDYRQSVSNV 120  
 DB 61 DFLVGLISIPLYIPIHVLFWNNFGSGICMFWLITDYLCTASVYVNLISDYRQSVSNV 120

QY 121 SYRAQHTGIMKIVAQVAVVILAFVNGPMLASDSWKNSNTKDCBFGFVTEWYILIT 180  
 DB 121 SYRAQHTGIMKIVAQVAVVILAFVNGPMLASDSWKNSNTKDCBFGFVTEWYILIT 180

QY 181 MLLEFLFVIVSVAYFNVQIYVNSLWKRRALSCPHAGSFSTSSASGHLHAGVACRTSN 240  
 DB 181 MLLEFLFVIVSVAYFNVQIYVNSLWKRRALSCPHAGSFSTSSASGHLHAGVACRTSN 240

QY 241 PGLKESAAHRSSEPRKSSILVSLRTHMNSSITAFKVGSPWRSAAALROREVAELLRG 300  
 DB 241 PGLKESAAHRSSEPRKSSILVSLRTHMNSSITAFKVGSPWRSAAALROREVAELLRG 300

QY 301 RKLARSAILLSAFACWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPLY 360  
 DB 301 RKLARSAILLSAFACWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPLY 360

QY 361 PLCHRRFQKAPWKILCVTK 379  
 DB 361 PLCHRRFQKAPWKILCVTK 379

RESULT 2  
 Q91ZY1 PRELIMINARY; PRT; 391 AA.  
 AC Q91ZY1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2003 (TrEMBLrel. 24, Last sequence update)  
 DE Histamine H4 receptor.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
 RT "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor  
 RT suggests substantial species variation."  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; AF358860; AAK97381.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PR01726; HISTAMINEH4.  
 DR PROSITE; PS00237; G PROTEIN RECP\_F1\_1; 1.  
 DR PROSITE; PS0262; G PROTEIN RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 391 AA; 44023 MW; C707BA6E39CFED41 CRC64;

Query Match 8.4%; Score 33; DB 11; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-25;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 KIVAQMVAWVILAFVNGPMLASDSWKNSNT 163  
 DB 131 KIVAQMVAWVILAFVNGPMLASDSWKNSNT 163

Db 131 KIVAQMVAWVILAFVNGPMLASDSWKNSNT 163

RESULT 3  
 Q91ZY1 PRELIMINARY; PRT; 389 AA.  
 AC Q91ZY1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Histamine H4 receptor.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
 RT "Comparison of human, mouse, rat, and guinea pig histamine H4 receptor  
 RT suggests substantial species variation."  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; AF358858; AAK97379.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR008102; Histamine\_H4.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PR01726; HISTAMINEH4.  
 DR PROSITE; PS00237; G PROTEIN RECP\_F1\_1; 1.  
 DR PROSITE; PS0262; G PROTEIN RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 389 AA; 44511 MW; 51AF32d6F1C3E4F CRC64;

Query Match 8.2%; Score 32; DB 11; Length 389;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-24;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 FWLITDYLCTASVYVNLISDYRQSVSNV 120  
 DB 88 FWLITDYLCTASVYVNLISDYRQSVSNV 119

RESULT 4  
 Q96LD9 PRELIMINARY; PRT; 390 AA.  
 AC Q96LD9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Histamine receptor H4.  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nguyen T., George S.R., Lee D.K., Cheng R., Lynch K.R., O'Dowd B.F.;  
 RT "Discovery of H4, a Novel Histamine Receptor."  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; AY008280; AAL09297.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.



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DR InterPro: IPR008102; Histamine_H4.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR01726; HISTAMINEH4R.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 390 AA; 44469 MW; CC82BD5D30D216C66 CRC64;

Query Match
Best Local Similarity 5.4%; Score 21; DB 4; Length 390;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 TDYLLCTASVYNIVLSIDRY 113
DB 93 TDYLLCTASVYNIVLSIDRY 113

RESULT 5
ID Q8WNV9 PRELIMINARY; PRT; 390 AA.
AC Q8WNV9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histamine H4 receptor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Oda T., Morikawa N., Saito Y., Masuho Y., Matsumoto S.;
RT "cDNA cloning and characterization of porcine histamine H4 receptor.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DE EMBL: A8053300; BAB83078.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR01726; HISTAMINEH4R.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 390 AA; 44483 MW; BC8FD363A6F44D3F CRC64;

Query Match
Best Local Similarity 4.1%; Score 16; DB 6; Length 390;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 DYLLCTASVYNIVLS 109
DB 96 DYLLCTASVYNIVLS 111

RESULT 6
ID Q865E3 PRELIMINARY; PRT; 147 AA.
AC Q865E3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histamine receptor H3 (Fragment).
GN HRH3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Witte D.G., Esbenshade T.A., Hancock A.A., Yao B.B.;
RT "The canine histamine receptor H3 (HRH3) partial cDNA sequence.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY231115; AAC83755.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004969; F:histamine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR003980; H3_receptor.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR01471; HISTAMINEH3R.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
KW NON_TER 1
FT NON_TER 147
FT NON_TER 147
SQ SEQUENCE 147 AA; 16900 MW; 67F6A741B518B54E CRC64;

Query Match
Best Local Similarity 2.8%; Score 11; DB 6; Length 147;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LNLAISDFLVG 65
DB 3 LNLAISDFLVG 13

RESULT 7
ID Q8NI50 PRELIMINARY; PRT; 200 AA.
AC Q8NI50;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Histamine H3 receptor isoform 5.
GN HRH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Neuropharmacology 0:0-0(2002).
DR EMBL: AF346903; BAM43828.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004969; F:histamine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR003980; H3_receptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR01471; HISTAMINEH3R.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
SQ SEQUENCE 200 AA; 21612 MW; 2038D14BC186D1EA CRC64;

Query Match
Best Local Similarity 2.8%; Score 11; DB 4; Length 200;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

ID Q8WXZ9 PRELIMINARY; PRT; 373 AA.  
AC Q8WXZ9  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Histamine H3 receptor isoform 4.  
GN HRH3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hippocampus;  
RA Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,  
RA Weiner D.M.;  
RT "Molecular Cloning and Characterization of Functionally Distinct  
RT Isoforms of the Human Histamine H3 Receptor.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF321913; AAL71914.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004969; F:histamine receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR000276; GPCR Rhodpsn.  
DR InterPro; IPR003980; H3\_receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PRINTS; PR01471; HISTAMINEH3.  
DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS00262; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 373 AA; 41570 MW; FAE9DFC5C3AF4DE9 CRC64;  
  
Query Match 2.8%; Score 11; DB 4; Length 373;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 55 LNLAISDFLVG 65  
Db 74 LNLAISDFLVG 84  
|||||  
RESULT 12  
Q865E1 PRELIMINARY; PRT; 445 AA.  
ID Q865E1  
AC Q865E1  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Histamine receptor H3.  
GN HRH3.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC EMBL; AY231164; AAO63757.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004969; F:histamine receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR000276; GPCR Rhodpsn.  
DR InterPro; IPR003980; H3\_receptor.  
DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.  
DR PRINTS; PR01471; HISTAMINEH3.  
DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS00262; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 445 AA; 48591 MW; E79440A4EC09CA8C CRC64;  
  
Query Match 2.8%; Score 11; DB 6; Length 445;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 55 LNLAISDFLVG 65  
Db 74 LNLAISDFLVG 84  
|||||  
RESULT 13  
Q84FJ1 PRELIMINARY; PRT; 79 AA.  
ID Q84FJ1  
AC Q84FJ1  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Putative root hair defective 3 protein (Fragment).  
OS Gossypioideis kirkii.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Gossypioideis.  
OX NCBI\_TaxID=47615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22569057; PubMed=12679546;  
RA Sanchina D.S., Alvarez I., Cronn R.C., Liu B., Rong J., Noyes R.D.,  
RA Paterson A.H., Wing R.A., Wilkins T.A., Wendel J.F.;  
RT "Rate variation among nuclear genes and the age of polyploidy in  
RT Gossypium.";  
RL Mol. Biol. Evol. 20:633-643(2003).  
DR EMBL; AY117084; AAM78203.1; -.  
DR NON TER 1  
SQ SEQUENCE 79 AA; 8010 MW; 03EE726CE662AC24 CRC64;  
  
Query Match 2.0%; Score 8; DB 10; Length 79;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 219 STTSSSAS 226  
Db 53 STTSSSAS 60  
|||||  
RESULT 14  
Q9F130 PRELIMINARY; PRT; 150 AA.  
ID Q9F130  
AC Q9F130  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Transposase subunit.  
GN TNPAL.  
OS Pseudomonas alcaligenes.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=43263;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NCIB 9867;  
RA Feng Y.M., Yeo C.C., Poh C.L.;  
RT "Cloning and characterization of gentisate 1,2-dioxygenase from  
RT Pseudomonas alcaligenes NCIB 9867.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF173167; AAG39456.1; -.  
DR InterPro; IPR002559; Transposase\_11.  
DR Pfam; PF01609; Transposase\_11; 1.

Mon Oct 4 10:27:27 2004

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SQ SEQUENCE 150 AA; 17439 MW; 8AAC59D07FD6E83B CRC64;
Query Match 2.0%; Score 8; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 CRTSNPGL 243
Db |||||
7 CRTSNPGL 14

RESULT 15
Q9BQJ4 PRELIMINARY; PRT; 181 AA.
AC Q9BQJ4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Brain cell membrane protein 1).
GN DKFZP761J17121.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amygdala;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiesmann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansgore W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RA "Towards a Catalog of Human Genes and Proteins: Sequencing and
RT Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
EL Genome Res. 11:422-435(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DDEJ databases.
DR EMBL; AL136550; CAB66485.1; -.
DR EMBL; BC039242; AAH39242.1; -.
RW Hypothetical protein.
SQ SEQUENCE 181 AA; 19997 MW; A73A03FD0C3B3FBB CRC64;

Query Match 2.0%; Score 8; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 FLVGLISI 69
Db |||||
96 FLVGLISI 103

Search completed: October 1, 2004, 10:28:58
Job time : 120 secs
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